WEST Search History

10/628,416

DATE: Wednesday, November 19, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=OR			
L1	polyadenylat$ near2 signal$	15532	L1
L2	polyadenylat$ near2 signal	15532	L2
L3	search or find	582585	L3
L4	l2 and l3	9890	L4
L5	(polyadenylat$ near2 signal) near5 (search or find or searching or finding)	11	L5
DB=USPT; PLUR=YES; OP=OR			
L6	L5	6	L6
DB=PGPB; PLUR=YES; OP=OR			
L7	L5	5	L7

Displayed KWIC w/o PR.

END OF SEARCH HISTORY

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NEWS1Web Page URLs for STN Seminar Schedule - N. America
NEWS2"Ask CAS" for self-help around the clock NEWS3SEP 09CA/CAplus records now contain indexing from 1907 to the present NEWS4AUG 05New pricing for EUROPATFULL and PCTFULL effective
August 1, 2003 NEWS5AUG 13Field Availability (/FA) field enhanced in BEILSTEIN NEWS6AUG 18Data available for download as a PDF in RDISCLOSURE NEWS7AUG 18Simultaneous left and right truncation added to PASCAL NEWS8AUG 18FROSTI and KOSMET enhanced with Simultaneous Left and Righ Truncation NEWS9AUG 18Simultaneous left and right truncation added to ANABSTR NEWS 10SEP 22DIPPR file reloaded NEWS 11DEC 08INPADOC: Legal Status data reloaded NEWS 12SEP 29DISSABS now available on STN NEWS 13OCT 10PCTFULL: Two new display fields added NEWS 14OCT 21BIOSIS file reloaded and enhanced NEWS 15OCT 28BIOSIS file segment of TOXCENTER reloaded and enhanced NEWS 16NOV 24MSDS-CCOHS file reloaded NEWS 17DEC 08CABA reloaded with left truncation NEWS 18DEC 08IMS file names changed NEWS 19DEC 09Experimental property data collected by CAS now available in REGISTRY NEWS 20DEC 09STN Entry Date available for display in REGISTRY and CA/CAplus
NEWS EXPRESSNOVEMBER 14 CURRENT WINDOWS VERSION IS V6.01c, CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP), AND CURRENT DISCOVER FILE IS DATED 23 SEPTEMBER 2003 NEWS HOURSSTN Operating Hours Plus Help Desk Availability NEWS INTERGeneral Internet Information NEWS LOGINWelcome Banner and News Items NEWS PHONEDirect Dial and Telecommunication Network Access to STN NEWS WWWCAS World Wide Web Site (general information)

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* * * * * * * * * * * * STNColumbus* * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 14:56:35 ON 15 DEC 2003

=>caplus
CAPLUS IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> s beaudoing/au
THIS COMMAND NOT AVAILABLE IN THE CURRENT FILE
Some commands only work in certain files.For example, the EXPAND
command can only be used to look at the index in a file which has an
index.Enter "HELP COMMANDS" at an arrow prompt (=>) for a list of
commands which can be used in this file.

=> file caplus
COST IN U.S. DOLLARS SINCE FILETOTAL
ENTRYSESSION
FULL ESTIMATED COST0.21 0.21

FILE 'CAPLUS' ENTERED AT 14:56:58 ON 15 DEC 2003
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FILE COVERS 1907 - 15 Dec 2003VOL 139 ISS 25
FILE LAST UPDATED: 14 Dec 2003(20031214/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s beaudoing/au
L1 0 BEAUDOING/AU

=> s smith/au
L2 5 SMITH/AU

=> e beaudoing/au
E139 BEAUDOIN Y/AU
E2 3 BEAUDOIN YVES/AU
E3 0 --> BEAUDOING/AU
E4 2 BEAUDOING A/AU
E5 5 BEAUDOING EMMANUEL/AU
E610 BEAUDOING G/AU
E7 1 BEAUDOING GEORGES/AU
E8 1 BEAUDOING MICHEL/AU
E9 1 BEAUDON C M/AU
E101 BEAUDONI GEORGES/AU
E11 11 BEAUDONNET A/AU
E122 BEAUDONNET ANDREE/AU

=> s e4-e8 2 "BEAUDOING A"/AU 5 "BEAUDOING EMMANUEL"/AU
10 "BEAUDOING G"/AU 1 "BEAUDOING GEORGES"/AU 1 "BEAUDOING MICHEL"/AU
L319 ("BEAUDOING A"/AU OR "BEAUDOING EMMANUEL"/AU OR "BEAUDOING G"/AU
OR "BEAUDOING GEORGES"/AU OR "BEAUDOING MICHEL"/AU)

=> s l3 and 2000/py 1014147 2000/PY

L4 2 L3 AND 2000/PY

=> d l4 1-2 bib ab

L4 ANSWER 1 OF 2CAPLUSCOPYRIGHT 2003 ACS on STN
AN 2000:515036CAPLUS
DN 133:359656
TI Patterns of variant polyadenylation signal usage in human genes
AU ***Beaudoing, Emmanuel***; Freier, Susan; Wyatt, Jacqueline R.; Claverie, Jean-Michel; Gautheret, Daniel
CS Structural and Genetic Information Laboratory, CNRS UMR 1889, Marseille, 13402, Fr.
SO Genome Research (***2000***), 10(7), 1001-1010 CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB The formation of mature mRNAs in vertebrates involves the cleavage and polyadenylation of the pre-mRNA, 10-30 nt downstream of an AAUAAA or AUUAAA signal sequence.The extensive cDNA data now available shows that these hexamers are not strictly conserved.In order to identify variant polyadenylation signals on a large scale, we compared over 8700 human 3' untranslated sequences to 157,775 polyadenylated expressed sequence tags (ESTs), used as markers of actual mRNA 3' ends.About 5600 EST-supported putative mRNA 3' ends were collected and analyzed for significant hexameric sequences.Known polyadenylation signals were found in only 73% of the 3' fragments.Ten single-base variants of the AAUAAA sequence were identified with a highly significant occurrence rate, potentially representing 14.9% of the actual polyadenylation signals.Of the mRNAs, 28.6% displayed two or more polyadenylation sites.In these mRNAs, the poly(A) sites proximal to the coding sequence tend to use variant signals more often, while the 3'-most site tends to use a canonical signal.The av. no. of ESTs assocd. with each signal type suggests that variant signals (including the common AUUAAA) are processed less efficiently than the canonical signal and could therefore be selected for regulatory purposes.However, the position of the site in the untranslated region may also play a role in polyadenylation rate.
RE.CNT60THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 2CAPLUSCOPYRIGHT 2003 ACS on STN
AN 2000:373551CAPLUS
DN 133:118912
TI Size estimate of the .alpha..beta. TCR repertoire of naive mouse splenocytes
AU Casrouge, Armanda; ***Beaudoing, Emmanuel***; Dalle, Sophie; Pannetier, Christophe; Kanellopoulos, Jean; Kourilsky, Philippe
CS Unite de Biologie Moleculaire du Gene, Institut National de la Sante et de la Recherche Medicale, Unite 277, Institut Pasteur, Paris, 75724, Fr.
SO Journal of Immunology (***2000***), 164(11), 5782-5787 CODEN: JOIMA3; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
AB The diversity of the T cell repertoire of mature T splenocytes is generated, in the thymus, by pairing of .alpha. and .beta. variable domains of the .alpha..beta. TCR and by the rearrangements of various gene segments encoding these domains.In the periphery, it results from competition between various T cell subpopulations including recent thymic migrants and long-lived T cells.Quant. data on the actual size of the T cell repertoire are lacking.Using PCR methods and extensive sequencing, we have measured for the first time the size of the TCR-.alpha..beta. repertoire of naive mouse T splenocytes.There are 5-8 .times. 105 different nucleotide sequences of BV chains in the whole spleen of young adult mice.We have also detd. the size of the BV repertoire in a subpopulation of AV2+ T splenocytes, which allows us to provide a min. est. of the .alpha..beta. repertoire.We find that the mouse spleen harbors about 2 .times. 106 clones of about 10 cells each.This figure, although orders of magnitude smaller than the max. theor. diversity (estd. up to 1015), is still large enough to maintain a high functional diversity.
RE.CNT34THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> log y
COST IN U.S. DOLLARS SINCE FILETOTAL
ENTRYSESSION
FULL ESTIMATED COST 19.8620.07

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILETOTAL
ENTRYSESSION
CA SUBSCRIBER PRICE -1.30-1.30

STN INTERNATIONAL LOGOFF AT 14:59:01 ON 15 DEC 2003

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NEWS EXPRESS NOVEMBER 14 CURRENT WINDOWS VERSION IS V6.01c, CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP), AND CURRENT DISCOVER FILE IS DATED 23 SEPTEMBER 2003 NEWS HOURS STN Operating Hours Plus Help Desk Availability NEWS INTER General Internet Information NEWS LOGIN Welcome Banner and News Items NEWS PHONE Direct Dial and Telecommunication Network Access to STN NEWS WWW CAS World Wide Web Site (general information)

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FILE 'HOME' ENTERED AT 12:49:17 ON 19 NOV 2003

=> le caplus
LE IS NOT A RECOGNIZED COMMAND
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=> file caplus
COST IN U.S. DOLLARS SINCE FILE TOTAL ENTRY SESSION
FULL ESTIMATED COST 0.21 0.21

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FILE COVERS 1907 - 19 Nov 2003 VOL 139 ISS 21
FILE LAST UPDATED: 18 Nov 2003 (20031118/ED)
This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s (polyadenylat? (2a) signal?)/bi,ab 10433
POLYADENYLAT?/BI 7977 POLYADENYLAT?/AB 470794
SIGNAL?/BI 426383 SIGNAL?/AB
L1 3018 (POLYADENYLAT? (2A) SIGNAL?)/BI,AB

=> s (search? or find?)/bi,ab 92365 SEARCH?/BI 75552
SEARCH?/AB 428530 FIND?/BI 421218 FIND?/AB
L2 514352 (SEARCH? OR FIND?)/BI,AB

=> s l1 and l2
L3 168 L1 AND L2

=> s l3 not 2003/py 942359 2003/PY
L4 156 L3 NOT 2003/PY

=> s l4 not 2002/py 1105706 2002/PY

L5 140 L4 NOT 2002/PY

=> s ((polyadenyl? (2a) signal?) (5a) (search? or find?))/bi,ab
11688 POLYADENYL?/BI 9170 POLYADENYL?/AB 470794
SIGNAL?/BI 426383 SIGNAL?/AB 92365 SEARCH?/BI 75552
SEARCH?/AB 428530 FIND?/BI 421218 FIND?/AB

L6 3 ((POLYADENYL? (2A) SIGNAL?) (5A) (SEARCH? OR FIND?))/BI,AB

=> d l6 1-3 bib ab

L6 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:20845 CAPLUS
DN 130:192448
TI Homology-based gene prediction using neural nets
AU Cai, Yudong; Bork, Peer
CS EMBL, Heidelberg, 690 12, Germany
SO Analytical Biochemistry (1998), 265(2), 269-274 CODEN: ANBCA2; ISSN: 0003-2697
PB Academic Press
DT Journal
LA English
AB We have developed and implemented a method for computational gene identification called GIN (gene identification using neural nets and homol. information) that has been particularly designed to avoid false pos. predictions. It thus predicts 55% of all genes tested correctly, has a specificity of 99%, but also has an overall accuracy of 92% on a benchmark set of 570 vertebrate genes constructed by Burset and Guigo. The method combines homol. searches in protein and expressed sequence tag databases with several neural networks designed to recognize start codons, Poly(A) signals, stop codons, and splice sites. Predicted exons are assembled into genes using a homol.-based scoring function. GIN is able to recognize multiple genes within genomic DNA as demonstrated by the identification of a globin gene (.gamma.-globin-1 (G)) that has not been annotated

as a coding region in the widely used the test set of Burset and Guigo. Furthermore, GIN identifies more than 107 other protein hits in noncoding regions and classifies them into possible pseudogenes or splice variants. (c) 1998 Academic Press.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:347889 CAPLUS
DN 127:61542
TI Regulation of tRNA suppressor activity by an intron-encoded polyadenylation signal
AU Liang, Songlin; Briggs, Michael W.; Butler, J. Scott
CS Department Microbiology Immunology, University Rochester School Medicine Dentistry, Rochester, NY, 14618, USA
SO RNA (1997), 3(6), 648-659 CODEN: RNARFU; ISSN: 1355-8382
PB Cambridge University Press
DT Journal
LA English
AB A 26-nt sequence from the 3' UTR of the yeast GAL7 mRNA directs accurate and efficient cleavage and polyadenylation to form the 3' end of the GAL7 mRNA in vivo and in vitro. Here we asked whether this polyadenylation signal can function within the context of a tRNA. Insertion of the GAL7 signal into the intron of the dominant SUP4 nonsense suppressor allowed us to judge the effect of the insert on SUP4 function by observation of nonsense suppression efficiency in vivo. The GAL7 signal impairs the function of SUP4 in an orientation-dependent manner in vivo, consistent with its ability to specify cleavage and polyadenylation in this context in vitro. Mutation of a UA repeat within the GAL7 signal restores SUP4 function partially, consistent with the role of this repeat as an efficiency element in polyadenylation. Mutations that impair the mRNA 3' end-processing factors Rna14p and Rna15p restore suppressor function partially. Northern blot anal., PCR amplification, and DNA sequence anal. show that the GAL7 signal directs polyadenylation within the body of pre-SUP4 and within the terminator, suggesting that polyadenylation inhibits 5' and 3' end processing, as well as removal of the pre-tRNA intron. These ***findings*** indicate that the GAL7 ***polyadenylation*** ***signal*** is capable of targeting a pre-tRNA to the mRNA processing pathway.

L6 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1985:56934 CAPLUS
DN 102:56934
TI Nucleotide sequence of an immediate-early frog virus 3 gene
AU Willis, Dawn; Foglesong, David; Granoff, Allan
CS St. Jude Child. Res. Hosp., Memphis, TN, 38101, USA
SO Journal of Virology (1984), 52(3), 905-12 CODEN: JOVIAM; ISSN: 0022-538X
DT Journal
LA English
AB Gene walking with synthetic oligonucleotides and phage M13 dideoxynucleotide sequencing techniques were used to obtain the complete coding and flanking sequences of the gene encoding a major immediate-early RNA (mol. wt., 169,000) of frog virus 3. R-loop mapping of the cloned XbaI K fragment of frog virus 3 DNA with immediate-early RNA from infected cells showed that an RNA of .apprx.500-600 nucleotides (the right size to code for the immediate-early viral 18-kilodalton protein of unknown function) hybridized to a region within 100 base pairs of 1 end of the XbaI K fragment; no evidence for splicing was obsd. in the electron microscope or by single-strand nuclease anal. Further restriction mapping narrowed the location of the gene to the XbaI end of a 2-kilobase-pair XbaI-BglII fragment, which was bidirectionally subcloned into the phage pair mp10 and mp11 for sequencing. Mung bean nuclease mapping was used to identify both the 5' and the 3' ends of the mRNA. The 5' end mapped within an AT-rich region 19 base pairs (bp) upstream from 2 in-phase AUG start codons that were immediately followed by an open reading frame of 157 amino acids. Another AT-rich sequence was found at -29 bp from the 5' end of the mRNA start site; this sequence may function as a TATA box. The 3' end of the message displayed considerable microheterogeneity, but clearly terminated within a 3rd AT-rich region 50-60 bp from the translation stop codon. The eukaryotic ***polyadenylic*** acid addn. ***signal*** (AATAAA) was not present, a ***finding*** to be expected since frog virus 3 mRNA is not polyadenylated. Both the single-stranded mp10 clone of the XbaI-BglII fragment and a 15-base oligonucleotide complementary to the region flanking the 2 AUG translation start codons inhibited translation of the immediate-early 18-kilodalton protein in vitro, confirming the identity of the sequenced gene. Whereas the regulatory sequences of this gene did not resemble those of known eukaryotic genes or of the cytoplasmic vaccinia virus, frog virus 3 has, apparently, evolved unique signals for the initiation and termination of transcription.

=> d his
(FILE 'HOME' ENTERED AT 12:49:17 ON 19 NOV 2003)
FILE 'CAPLUS' ENTERED AT 12:49:27 ON 19 NOV 2003
L1 3018 S (POLYADENYLAT? (2A) SIGNAL?)/BI,AB
L2 514352 S (SEARCH? OR FIND?)/BI,AB
L3 168 S L1 AND L2
L4 156 S L3 NOT 2003/PY

L5 140 S L4 NOT 2002/PY

L6 3 S ((POLYADENYL? (2A) SIGNAL?) (5A) (SEARCH? OR FIND?))/BI,AB

=> s l5 1-140 bib ab
MISSING OPERATOR L5 1-140
The search profile that was entered contains terms or nested terms that are not separated by a logical operator.

=> d l5 1-140 bib ab

L5 ANSWER 1 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2002:744556 CAPLUS
DN 138:101589
TI Cloning of a transmissible gastroenteritis coronavirus full-length cDNA
AU Gonzalez, Jose M.; Almazan, Fernando; Penzes, Zoltan; Calvo, Enrique; Enjuanes, Luis
CS Department of Molecular and Cell Biology, Centro Nacional de Biotecnologia, CSIC, Madrid, 28049, Spain
SO Advances in Experimental Medicine and Biology (2001), 494(Nidoviruses (Coronaviruses and Arteriviruses)), 533-536 CODEN: AEMBAP; ISSN: 0065-2598
PB Kluwer Academic/Plenum Publishers
DT Journal
LA English
AB To understand gene function and expression in coronaviruses it would be of interest to obtain a cDNA encoding a full-length infectious RNA. In this report we describe the construction of a transmissible gastroenteritis virus (TGEV) full-length cDNA. For this purpose, we started from a cDNA encoding the defective RNA DI-C. During the completion of the cDNA an ORF 1a fragment that was toxic to the bacteria was identified. Advantage of this ***finding*** was taken by reintroducing the toxic fragment into the viral cDNA in the last cloning step. To enhance

the stability of the viral sequence, the cDNA was cloned as a bacterial artificial chromosome (BAC). The cytomegalovirus (CMV) immediate-early promoter was placed upstream of the cDNA to make use of a two-step amplification system that couples RNA pol II-driven transcription in the nucleus with the amplification by the viral replicase in the cytoplasm.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:838962 CAPLUS
DN 137:42296
TI Transgenic mice carrying a gene for green fluorescent protein fused to a lytic peptide, Shiva 1, under control of the bovine .beta.-casein regulatory region
AU Thonabulsombat, Charoensri; Reed, William A.; Morrey, John D.; Bates, Katherine; Smart, Ross A.; White, Kenneth L.
CS Department of Animal, Dairy and Veterinary Sciences, Biotechnology Center, Utah State University, Logan, UT, 84322-4700, USA
SO Transgenics (2001), 3(2-4), 183-197 CODEN: TADTEF; ISSN: 1023-6171
PB Harwood Academic Publishers
DT Journal
LA English
AB The synthesis of foreign proteins can be targeted to the mammary gland of transgenic animals. In this study, the expression vector consisted of a gene for an amphipathic lytic peptide (Shiva 1) fused to green fluorescent protein (GFP) controlled by the bovine .beta.-casein promoter and enhancer. The regulatory elements included exons, introns, and the ***polyadenylation*** ***signal*** . A 4.5 kb fragment of the 5' region and a 2.2 kb fragment of the 3' region were isolated by polymerase chain reaction (PCR). The plasmid, pCas-GFP-Shiva-Cas, allowed transcription and processing of mRNA for a fusion peptide that included the secretory signal sequence from the bovine .beta.-casein, a linker peptide, green fluorescent protein, and Shiva 1. A fragment contg. the structural gene and the 5' and 3' flanking regions of .beta.-casein was injected into the pronuclei of murine zygotes for the prodn. of transgenic mice. The resultant transgenic mice were identified by PCR. Mouse milk was analyzed by western blot using a polyclonal antibody against GFP. The concn. of the 32 kD GFP-Shiva 1 protein from milk was estd. to range from 40 to 80 mg ml-1 (1.250 .mu.M to 2.500 .mu.M) in transgenic mice, 12 to 25 fold higher than concns. of Shiva 1 known to be toxic to eukaryotic cells. All transgenic mice had morphol. and histol. normal mammary glands and raised pups to weaning without indication of toxicity. These ***findings*** demonstrate that a potentially toxic protein can be produced in the milk of transgenic animals.
RE.CNT 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 3 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:599623 CAPLUS
DN 136:195083
TI Cloning of a novel mouse Gabarapl2 cDNA and its characterization
AU Chen, Zheng; Xin, Yu-Rong; Jiang, Ying; Jiang, Ju-Xiang
CS School of Life Science, Suzhou University, Suzhou, 215006, Peop. Rep. China
SO Acta Pharmacologica Sinica (2001), 22(8), 751-755 CODEN: APSCG5
PB Science Press
DT Journal
LA English
AB Aim: To clone a novel mouse GABAA-receptor-assocd. protein like 2 (Gabarapl2) gene, and to anal. its primary function. Methods: With the aid of computer, the human GABARAPL2 cDNA was used as information probe to ***search*** mouse EST database of GenBank for mouse homolog. A series of overlapping EST were found and assembled into an EST contig using Genetics Computer Group (GCG) ASSEMBLY program. The existence of the gene was then identified by expt. Northern blotting was performed to hybridize [.alpha.-32P]dATP labeled probe with mRNA of 11 different mouse tissues that had been transferred to the nylon membrane. Results: The novel gene was deposited in GenBank under Accession No AF190644. Its cDNA contained an intact open reading frame and a canonical ***polyadenylation*** ***signal*** AATAAA followed by polyA. The deduced protein was completely identical to that of human GABARAPL2, and was termed Gabarapl2 by Mouse Gene Nomenclature Committee. The putative protein of Gabarapl2 has a calcd. mol. wt. of 13 700 and an isoelec. point of 8.56. It was also predicted to contain two protein kinase C phosphorylation sites and one tyrosine kinase phosphorylation site. Northern hybridization showed that Gabarapl2 was expressed as a single 1.35 kb transcript, with high levels in brain, thymus, lung, heart, kidney, and liver, and low in pancreas, testis, small intestine, colon, and stomach. Conclusion: A novel mouse Gabarapl2 gene was cloned and identified.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 4 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:581239 CAPLUS
DN 135:270470
TI Gene expression of D-amino acid oxidase in nervous system
AU Kanamori, T.; Obayashi, M.; Jinnouchi, O.; Kanda, K.; Urai, Y.; Shishido, Y.; Suzue, A.; Sakai, T.; Fukui, K.
CS The Institute for Enzyme Research, The University of Tokushima, Tokushima, Japan
SO Flavins and Flavoproteins 1999, Proceedings of the International Symposium, 13th, Konstanz, Germany, Aug. 29-Sept. 4, 1999 (1999), 887-890. Editor(s): Ghisla, Sandro. Publisher: Rudolf Weber, Agency for Scientific Publications, Berlin, Germany. CODEN: 69BQDP
DT Conference
LA English
AB In this study, in ***search*** of nervous system specific expression of D-amino acid oxidase (DAO), reverse transcriptase-coupled PCR (polymerase chain reaction) analyses were carried out to confirm the gene expression of DAO in brain and then we have cloned the rat cerebellar cDNA and predicted the primary structure of DAO expressed in the nervous tissue. The mRNA for DAO was found in cerebellum. Anal. of the nucleotide (nt) sequence revealed that full length cDNA has a 1547 nt sequence with a 5'-untranslated region of 199 nt, an open reading frame of 1041 nt that encodes 346 amino acids, and 3'- untranslated region of 307 nt that contains the ***polyadenylation*** ***signal*** sequence. The deduced amino acid sequence consisting of 346 amino acids showed 93.1, 80.7, 77.8 and 79.0 % identity with the mouse, human, porcine and rabbit kidney enzymes, resp. Three catalytically important residues, Tyr-224, Tyr-228 and Arg-283, of the porcine enzyme were all conserved in theses 4 species. The targeting signal for the peroxisome localization of the brain enzyme was also present at the C-terminal sequence, Ser-His-Leu. The assignment of the initiation site of translation was based on the fact that ATG at 1-3 of the open reading frame was preceded by sequences that fulfill the Kozak criteria for initiation codon. A difference was obsd. in the no. of amino acid residues among the enzymes of animal species. Porcine, human and rabbit enzymes are encoded by 347 amino

acid residues, whereas mouse is 345. The N-terminal sequence comprising the first 30 amino acids of the rat cerebellar DAO was, like in the cases of other DAOs, highly hydrophobic, and contains a sequence characteristic of a FAD binding site, Gly-X-Gly-X-X-Gly. The C-terminal tripeptide peroxisomal targeting signal sequence, Ser-His-Leu, is also conserved in cerebellar DAO, indicating the presence of DAO in peroxisomes in nervous tissues. Based on these data, the primary structure of the brain enzyme is identical with that of the kidney enzyme, encoded by the same single gene in the genome. We postulate that DAO expressed in the brain astrocytes may be the key enzyme metabolizing D-serine, an allosteric modulator of NMDA receptor, as summarized schematically.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:506017 CAPLUS
DN 136:162103
TI Cloning and sequence analysis of Gpdh in Callosobruchus chinensis (Coleoptera: Bruchidae)
AU Park, Kwang-Sook; Bae, Young-Joo; Yeau, Sung-Hee; Kang, Soon-Ja
CS Department of Microbiology and Institute for Viral Disease, Medical College, Korea University, Seoul, 136-705, S. Korea
SO Molecules and Cells (2001), 11(3), 405-410 CODEN: MOCEEK; ISSN: 1016-8478
PB Springer-Verlag Singapore Pte. Ltd.
DT Journal
LA English
AB The Sn-Glycerol-3-phosphate dehydrogenase (GPDH: NAD+ 2-oxidoreductase, EC 1.1.1.8) gene of C. chinensis was cloned and its nucleotide sequence was analyzed. The gene was obtained by screening a genomic library with Drosophila melanogaster Gpdh and PCR amplification. The 5,126 bp gene obtained is comprised of one 5' untranslated region, eight exons, seven introns, and three 3' untranslated regions. Comparison of Gpdh of D. melanogaster with that of C. chinensis showed a 89.9% identity in the coding region, 70% in the intron, 79% in the entire nucleotide sequence, and 83.2% in the deduced amino acid sequence. The transcription initiation site is located 33 nucleotides upstream of the initiation codon, and the sequence anal. of the promoter region showed TATA and CAAT boxes at the 5' end. The stop codon (TAA) and ***polyadenylation*** ***signal*** (AATAAA) are located at the 3' end of each of the exons 6 to 8. These ***findings*** show that GPDH isoenzymes in C. chinensis are produced by the alternative processing of 3' exons. The occurrence of the three transcripts was proven by RT-PCR using synthetic oligonucleotides complementary to the predicted unique 3' regions. Compared to the D. melanogaster GPDH isoenzymes, GPDH-1, -2, and -3, C. chinensis GPDH showed 83.6%, 83%, and 84% identities, resp.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 6 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:395433 CAPLUS
DN 135:117318
TI Genomic structure and transcriptional regulation of the human growth hormone secretagogue receptor
AU Petersenn, Stephan; Rasch, Anja C.; Penshorn, Martina; Beil, Frank U.; Schulte, Heinrich M.
CS IHF Institute for Hormone and Fertility Research, University of Hamburg, Hamburg, 22529, Germany
SO Endocrinology (2001), 142(6), 2649-2659 CODEN: ENDOAO; ISSN: 0013-7227
PB Endocrine Society
DT Journal
LA English
AB Synthetic GH secretagogues stimulate GH release through binding to a recently cloned specific GH secretagogue receptor (GHS-R). The endogenous ligand of this receptor may be part of a new endocrine pathway controlling GH secretion. Two different receptor variants, type 1a and 1b, have been described that differ in their 3'-terminal amino acids. The authors investigated the genomic structure and transcriptional regulation of the human GHS-R. An 18-kb genomic clone including sequences encoding for the two GHS-R variants was isolated. Sequencing revealed that the two variants originate from specific RNA processing of a single gene that spans approx. 4.1 kb. The transcription start site was defined by 5'-inverse PCR anal. at position - 227. RT-PCR anal. points to differential transcriptional initiation and processing. Type 1a is encoded by two exons; 2152 bp of intronic sequence are removed by splicing at position 796/797 relative to the translation start site. Type 1b is encoded by a single exon. A putative ***polyadenylation*** ***signal*** consensus motif was identified at position +4118; 2.7 kb of the 5'-flanking region were sequenced, and putative transcription factor binding sites were identified. Transcriptional regulation was investigated by transient transfections using promoter fragments ranging in size from 168-1745 bp; 1745 bp of the GHS-R promoter directed significant levels of luciferase expression in GH4 rat pituitary cells, whereas no activity was detected in monkey kidney COS-7 cells, human endometrium Skut-1B cells, mouse hypothalamic LHRH neuronal GT1-7 cells, or mouse corticotroph pituitary AtT20 cells. A minimal 309-bp promoter allowed pituitary-specific expression. Its activity in COS-7 cells was enhanced by cotransfection of the pituitary-specific transcription factor Pit-1. The authors did not ***find*** any regulation of the GHS-R promoter by forskolin, somatostatin, insulin-like growth factor I, or 12-O-tetraphorbol 12-myristate 13-acetate. Thyroid hormone and estrogen lead to a significant stimulation; glucocorticoids lead to a significant inhibition. Further mapping suggests a thyroid hormone-responsive element, an estrogen-responsive element, and a glucocorticoid-responsive element located between - 309 and the translation start codon. These studies demonstrate the nature of the human GHS-R gene and identify its 5'-flanking region. Furthermore, pituitary-specific activity of the promoter and regulation by various hormones are demonstrated.
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 7 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:223797 CAPLUS
DN 136:15789
TI Characterization of a cytokinin induced cDNA showing sequence homologies to hybrid proline (or glycine) rich proteins in Catharanthus roseus cell suspension cultures
AU Chahed, Karim; Limam, Ferid; Gargouri, Ali; Ghrir, Rachid; Ouelhazi, Lazhar
CS Laboratoire de Biochimie Vegetale, Institut National de la Recherche Scientifique et Technique, Hammam-Lif, 2050, Tunisia
SO Acta Botanica Gallica (2000), 147(4), 311-321 CODEN: ABGAE9; ISSN: 1253-8078
PB Societe Botanique de France
DT Journal
LA English
AB In a preliminary screening of a cDNA library we isolated a cDNA that accumulates to high levels in cytokinin treated cells. The expression of the related transcript was induced after treatment with benzylaminopurine (BAP), zeatine and kinetine. Sequence anal. showed the presence of multiple initiation and stop codons and the absence of a long open reading frame

(ORF). However, classic ***polyadenylation*** ***signals*** and poly A tail were found. ***Searching*** for nucleotide and amino acid similarities revealed a strong homol. (up to 90%) with cDNAs corresponding to hybrid proline (or glycine) - rich proteins (HyPRP/HyGRP). A particular homol. was found with a recently reported tobacco cDNA which encodes a novel glycine rich hydrophobic protein.
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 8 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:207699 CAPLUS
DN 135:299385
TI Nucleotide sequence of the mouse VEGF 3'UTR and quantitative analysis of sites of polyadenylation
AU Dibbens, J. A.; Polyak, S. W.; Damert, A.; Risau, W.; Vadas, M. A.; Goodall, G. J.
CS Division of Human Immunology, Hanson Centre for Cancer Research, IMVS, Adelaide, 5000, Australia
SO Biochimica et Biophysica Acta (2001), 1518(1-2), 57-62 CODEN: BBACAQ; ISSN: 0006-3002
PB Elsevier Science B.V.
DT Journal
LA English
AB Sequencing of rat and human vascular endothelial growth factor (VEGF) cDNA clones has previously identified a 3' untranslated region of approx. 1.9 kb, although the apparent site of polyadenylation differed in the two species, despite a high degree of sequence conservation in the region. Neither site is preceded by a canonical AAUAAA ***polyadenylation*** ***signal*** , a situation frequently found in genes that are subject to alternative polyadenylation. We have sequenced 2.25 kb of the 3' region of the mouse VEGF gene and mapped the usage of potential polyadenylation sites in fibroblasts cultured under both normoxic and hypoxic conditions. We ***find*** that two sites for polyadenylation are present in the mouse VEGF gene but the majority of transcripts contain the longer form of the 3'UTR and that their usage is not effected by environmental oxygen tension.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 9 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:196139 CAPLUS
DN 136:1358
TI Cloning and sequence of the gene encoding the muscle fatty acid binding protein from the desert locust, Schistocerca gregaria
AU Wu, Q.; Andolfatto, P.; Haunerland, N. H.
CS Department of Biological Sciences, Simon Fraser University, Burnaby, BC, V5A 1S6, Can.
SO Insect Biochemistry and Molecular Biology (2001), 31(6/7), 553-562 CODEN: IBMBES; ISSN: 0965-1748
PB Elsevier Science Ltd.
DT Journal
LA English
AB Muscle fatty acid binding protein (FABP) is a major cytosolic protein in flight muscle of the desert locust, Schistocerca gregaria. FABP expression varies greatly during development and periods of increased fatty acid utilization, but the mol. mechanisms that regulate its expression are not known. In this study, the gene coding for locust muscle FABP was amplified by PCR and cloned, together with 1.2 kb of upstream sequence. The sequence coding for the 607 bp cDNA is interrupted by two introns of 12.7 and 2.9 kb, inserted in analogous positions as the first and third intron of the mammalian homologues. Both introns contain repetitive sequences also found in other locust genes, and the second intron contains a GT-microsatellite. The promoter sequence includes a canonical TATA box 24 bp upstream of the transcription start site. The upstream sequence contains various potential myocyte enhancer sequences and a 160 bp segment that is repeated three times. In database ***searches*** in the genome database of Drosophila melanogaster, a gene with the same gene organization and promoter structure was identified, likely the dipteran homolog of muscle FABP. Upstream of both insect genes, a conserved 19 bp inverted repeat sequence was detected. A similar but reverse palindrome is also present upstream of all mammalian heart FABP genes, possibly representing a novel element involved in muscle FABP expression.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 10 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:154054 CAPLUS
DN 135:191229
TI Expressing the human genome
AU Tupler, Rossella; Perini, Giovanni; Green, Michael R.
CS Howard Hughes Medical Institute, Programs in Gene Function and Expression and Molecular Medicine, University of Massachusetts Medical School, Worcester, MA, 01605, USA
SO Nature (London, United Kingdom) (2001), 409(6822), 832-833 CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English
AB We have ***searched*** the human genome for genes encoding new proteins that may be involved in three nuclear gene expression processes: transcription, pre-mRNA splicing and polyadenylation. A plethora of potential new factors are implicated by sequence in nuclear gene expression, revealing a substantial but selective increase in complexity compared with Drosophila melanogaster and Caenorhabditis elegans. Although the raw genomic information has limitations, its availability offers new exptl. approaches for studying gene expression.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 11 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:80749 CAPLUS
DN 135:163306
TI Jule from the fish Xiphophorus is the first complete vertebrate Ty3/Gypsy retrotransposon from the Mag family
AU Volff, Jean-Nicolas; Korting, Cornelia; Altschmied, Joachim; Duschl, Jutta; Sweeney, Kimberley; Wichert, Katrin; Froschauer, Alexander; Schartl, Manfred
CS Physiological Chemistry I, Biocenter, University of Wurzburg, Wurzburg, D-97074, Germany
SO Molecular Biology and Evolution (2001), 18(2), 101-111 CODEN: MBEVEO; ISSN: 0737-4038
PB Society for Molecular Biology and Evolution
DT Journal
LA English
AB Jule is the second complete long-terminal-repeat (LTR) Ty3/Gypsy retrotransposon identified to date in vertebrates. Jule, first isolated from the poeciliid fish Xiphophorus maculatus, is 4.8 kb in length, is flanked by two 202-bp LTRs, and encodes Gag (structural core protein) and Pol (protease, reverse transcriptase, RNase H, and integrase, in that order) but no envelope. There are three to four copies of Jule per haploid genome in X. maculatus. Two of them are located in a subtelomeric region of the sex chromosomes, where they are assocd. with the Xmrk receptor tyrosine kinase genes, of which oncogenic versions are responsible for the formation of hereditary melanoma in Xiphophorus. One almost intact copy of Jule was found in the

first intron of the X-chromosomal allele of the Xmrk proto-oncogene, and a second, more corrupted copy is present only 56 nt downstream of the ***polyadenylation*** ***signal*** of the Xmrk oncogene. Jule-related elements were detected by Southern blot hybridization with less than 10 copies per haploid genome in numerous other poeciliids, as well as in more divergent fishes, including the medakafish Oryzias latipes and the tilapia Oreochromis niloticus. Database ***searches*** also identified Jule-related sequences in the zebrafish Danio rerio and in both genome project pufferfishes, Fugu rubripes and Tetraodon nigroviridis. Phylogenetic anal. revealed that Jule is the first member of the Mag family of Ty3/Gypsy retrotransposons described to date in vertebrates. This family includes the silkworm Mag and sea urchin SURL retrotransposons, as well as sequences from the nematode Caenorhabditis elegans. Addnl. related elements were identified in the genomes of the malaria mosquito Anopheles gambiae and the nematode Ascaris lumbricoides. Phylogeny of Mag-related elements suggested that the Mag family of retrotransposons is polyphyletic and is constituted of several ancient lineages that diverged before their host genomes more than 600 MYA.
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 12 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2001:39839 CAPLUS
DN 135:103232
TI Human EIF5A2 on chromosome 3q25-q27 is a phylogenetically conserved vertebrate variant of eukaryotic translation initiation factor 5A with tissue-specific expression
AU Jenkins, Zandra A.; Haag, Petra G.; Johansson, Hans E.
CS Department of Cell and Molecular Biology and Department of Genetics and Pathology, Uppsala University, Uppsala, SE-751 24, Swed.
SO Genomics (2001), 71(1), 101-109 CODEN: GNMCEP; ISSN: 0888-7543
PB Academic Press
DT Journal
LA English
AB Eukaryotic translation initiation factor 5A (eIF5A) is an essential protein tightly linked to cellular polyamine homeostasis. It receives the unique spermidine-derived posttranslational modification hypusine that is necessary for eIF5A's biochem. activity and cellular proliferation. The eIF5A protein stimulates ribosomal peptidyl-transferase and may be involved in nucleocytoplasmic mRNA transport. Little is known about the mol. genetics of eIF5A. Here we report on the sequence and mol. characterization of human EIF5A2, a novel phylogenetically conserved gene for eIF5A. EIF5A2 stretches over 17 kb and consists of five exons and four introns. It is localized at 3q25-q27, often noted for chromosomal instability in cancers. EIF5A2 is highly expressed in testis and colorectal adenocarcinoma and at moderate levels in the brain, in contrast to the ubiquitously expressed EIF5A1 gene. Two EIF5A2 mRNAs share a 129-nt 5' UTR and a coding sequence for the 153-amino-acid eIF5AII protein, but possess two alternative 3' UTRs of 46 and 890 nt that arise through differential polyadenylation. The protein is 84% identical and 94% similar to eIF5AI. Both EIF5A genes are conserved in vertebrates. Our ***findings*** lend further support for a specialized gene expression program of polyamine metabolic proteins and regulators that function to maintain polyamine homeostasis at elevated levels during spermatogenesis. (c) 2001 Academic Press.
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 13 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2000:721254 CAPLUS
DN 134:247788
TI The viral RNA 3'- and 5'-end structure and mRNA transcription of infectious salmon anaemia virus resemble those of influenza viruses
AU Sandvik, T.; Rimstad, E.; Mjaaland, S.
CS Department of Pharmacology, Microbiology and Food Hygiene, The Norwegian School of Veterinary Science, Oslo, Norway
SO Archives of Virology (2000), 145(8), 1659-1669 CODEN: ARVIDF; ISSN: 0304-8608
PB Springer-Verlag Wien
DT Journal
LA English
AB The nucleotide sequences of the termini of two of the genomic segments of the neg. strand RNA virus infectious salmon anemia virus (ISAV) were detd. The sequence of the terminal 9 nucleotides at both ends of the viral RNAs was identical, and showed distinctive sequence homol. with the conserved terminal sequences found in the orthomyxoviruses. For both ISAV genomic segments a computer-based secondary structure modeling indicated that the terminal 21-24 nucleotides were able to form self-complementary panhandle structures. Comparison with ISAV-derived mRNA sequences showed that ISAV mRNAs have heterogeneous 5'-ends and are ***polyadenylated*** from a ***signal*** sequence 13-14 nucleotides downstream of the 5'-end terminus of the vRNA. Furthermore, the in vitro replication of ISAV was hindered by the RNA polymerase II inhibitor .alpha.-amanitin. These ***findings*** indicate that the mechanisms for replication of ISAV are similar to those of the orthomyxoviruses, and add to the previously reported structural similarities between ISAV and the orthomyxoviruses.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 14 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2000:702961 CAPLUS
DN 134:173758
TI Premature polyadenylation contributes to the poor expression of the Bacillus thuringiensis cry3Ca1 gene in transgenic potato plants
AU Haffani, Y. Z.; Overney, S.; Yelle, S.; Bellemare, G.; Belzile, F. J.
CS Departement de Phytologie, Pavillon C.E. Marchand, Universite Laval, Quebec, QC, G1K7P4, Can.
SO Molecular and General Genetics (2000), 264(1-2), 82-88 CODEN: MGGEAE; ISSN: 0026-8925
PB Springer-Verlag
DT Journal
LA English
AB The cry genes that code for the insecticidal crystal proteins of Bacillus thuringiensis (B.t.) have been widely used to develop insect-resistant transgenic plants. The cry3Ca1 gene has been reported to code for a crystal protein which is particularly potent against the Colorado potato beetle (CPB). To explore the biotechnol. potential of cry3Ca1, we introduced this gene into transgenic potato plants under the control of the CaMV 35S promoter. In the resulting transformants, the cry3Ca1 gene was very poorly expressed. In fact, no full-length transcript (2300 nt) could be detected. Instead, only short transcripts of approx. 1100 nt were obsd. Anal. of these short transcripts by Northern hybridization, RT-PCR as well as by cloning and sequencing showed that they resulted from premature polyadenylation. These processing events occurred at four sites within the cry3Ca1 coding region (at positions 652, 669, 914 and 981 relative to the translation start site). The sites at which premature polyadenylation took place were not those that showed the highest degree of identity to the canonical AAUAAA motif.

Together with other recent data, our ***findings*** suggest that premature polyadenylation is an important mechanism which can contribute to the poor expression of transgenes in a foreign host.
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 15 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2000:548519 CAPLUS
DN 133:263027
TI Characterization of naturally occurring and recombinant human N-acetyltransferase variants encoded by NAT1*
AU De Leon, Jesus H.; Vatsis, Kostas P.; Weber, Wendell W.
CS Department of Pharmacology, Medical School, The University of Michigan, Ann Arbor, MI, USA
SO Molecular Pharmacology (2000), 58(2), 288-299 CODEN: MOPMA3; ISSN: 0026-895X
PB American Society for Pharmacology and Experimental Therapeutics
DT Journal
LA English
AB The genotype at the NAT1* locus of an interethnic population of 38 unrelated subjects was detd. by direct sequencing of 1.6-kb fragments amplified by PCR. The coding exon alone and together with the 3' noncoding exon of the wild-type (NAT1*4) and the three mutant alleles (NAT1*10, *11, and *16) detected was expressed in Escherichia coli and COS-1 cells, resp., and the cytosolic fraction of mononuclear leukocytes from NAT1*4/*4 and NAT1*10/*10 homozygotes was also isolated. Recombinant and leukocyte cytosolic prepns. were thoroughly characterized by N-acetylation activity with several NAT1-specific and -selective substrates, as well as by steady-state kinetics with varying amts. of the substrate (fixed acetyl CoA) and acetyl CoA (fixed substrate), thermodn., stability, and protein immunoreactivity with a polyclonal human anti-NAT1. The ***polyadenylation*** ***signal*** mutation in the 3' noncoding sequence of NAT1*10 affected none of the aforementioned parameters evaluated both with recombinant NAT1*10 and with the naturally occurring allele. Function was also unaffected by the coding and 3' noncoding exon mutations in NAT1*11. In contrast, the three extra adenosines located immediately after the sixth position of the ***polyadenylation*** ***signal*** in the 3' untranslated region of NAT1*16 ostensibly caused disruption of the predicted secondary structure of the pre-mRNA for NAT1 16, culminating in parallel 2-fold decreases in the amt. and catalytic activity of NAT1 16 in COS-1 cell cytosol. This novel ***finding*** in N-acetylation pharmacogenetics clearly demonstrates a direct link between reduced catalytic activity and structural alteration in the 3' untranslated region of an NAT variant (NAT1*16) brought about by mutation.
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 16 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2000:479103 CAPLUS
DN 134:203204
TI A new system for the in vivo study of mRNA ***polyadenylation*** ***signal*** sequences in yeast cells
AU Miloshev, G. A.; Venkov, P. V.
CS Department of Molecular Genetics Institute of Molecular Biology, Bulgarian Academy of Sciences, Sofia, 1113, Bulg.
SO Dokladi na Bulgarskata Akademiya na Naukite (1998), 51(1-2), 105-108 CODEN: DBANEH; ISSN: 0861-1459
PB Bulgarska Akademiya na Naukite
DT Journal
LA English
AB Most eukaryotic mRNAs have a polyadenylated sequence at the 3'-end which is added in a posttranscriptional process. In higher eukaryotes well defined sequences exist that are responsible for the proper polyadenylation of mRNA. The consensus motif for pre-mRNA ***polyadenylation*** ***signal*** in Saccharomyces cerevisiae is not yet defined. In this paper we report the development of a system suitable for studying polyadenylation in vivo. Heterologous histone H1 mRNA from sea-urchin (Psammechinus miliaris), which is not polyadenylated naturally, is polyadenylated when expressed in S. cerevisiae. This ***finding*** suggests that foreign histone H1 mRNA can be polyadenylated in yeast cells. Furthermore, the dependence of ***polyadenylation*** upon ***signal*** sequences and some of the functions of polyadenylation can be readily investigated in this system by deleting or inserting certain sequences.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 17 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2000:470291 CAPLUS
DN 134:69106
TI Human CKI.alpha.L and CKI.alpha.S are encoded by both 2.4- and 4.2-kb transcripts, the longer containing multiple RNA-destabilising elements
AU Yong, T. J. K.; Gan, Y.-Y.; Toh, B.-H.; Sentry, J. W.
CS Division of Biology, National Institute of Education, Nanyang Technological University, Singapore, Singapore
SO Biochimica et Biophysica Acta (2000), 1492(2-3), 425-433 CODEN: BBACAQ; ISSN: 0006-3002
PB Elsevier Science B.V.
DT Journal
LA English
AB Casein kinase I (CKI) are a family of conserved second messenger-independent serine/threonine protein kinases found in all eukaryotes. The avian and mammalian CKI alpha isoform has four splice variants differing in the presence or absence of 28 amino acids ('L' insertion) in the catalytic domain and/or 12 amino acids ('S' insertion) in the regulatory domain. Here we report the isolation of cDNAs encoding human CKI.alpha.L and CKI.alpha.S. We ***find*** human CKI.alpha.L has a preference to phosphorylate phosvitin over casein, with a higher Km for casein than phosvitin, the reverse being the case for human CKI.alpha.S. Both human CKI.alpha.L, and CKI.alpha.S are derived from 4.2-kb mRNA transcripts and 2.4-kb transcripts, the latter probably generated by use of an alternate ***polyadenylation*** ***signal*** identified in the longer transcripts. The 4.2-kb transcripts contain six RNA-destabilizing AU-rich element (ARE) motifs in the 3'-untranslated region (UTR), while the 2.4-kb transcripts contain a single ARE motif. In vitro anal. of CKI alpha 3'-UTR RNA sequences suggests that in HeLa cells, the longer 3'-UTR transcripts are likely to degrade approx. 13 times faster than the shorter 3'-UTR transcripts. This is the first report of a kinase mRNA contg. multiple RNA-destabilizing AREs in the longer of two mRNA transcripts.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 18 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2000:228614 CAPLUS
DN 132:344623
TI Functionally significant secondary structure of the simian virus 40 late ***polyadenylation*** ***signal***
AU Hans, Holly; Alwine, James C.
CS Department of Microbiology, Microbiology and Virology Graduate Program, School of Medicine, University of Pennsylvania, Philadelphia, PA, 19104-6142, USA
SO Molecular and Cellular Biology (2000), 20(8), 2926-2932 CODEN: MCEBD4; ISSN: 0270-7306

PB American Society for Microbiology
DT Journal
LA English
AB The structure of the highly efficient simian virus 40 late ***polyadenylation*** ***signal*** (LPA ***signal***) is more complex than those of most known mammalian ***polyadenylation*** ***signals*** . It contains efficiency elements both upstream and downstream of the AAUAAA region, and the downstream region contains three defined elements (two U-rich elements and one G-rich element) instead of the single U- or GU-rich element found in most ***polyadenylation*** ***signals*** . Since many reports have indicated that the secondary structure in RNA may play a significant role in RNA processing, we have used nuclease structure anal. techniques to det. the secondary structure of the LPA signal. We ***find*** that the LPA signal has a functionally significant secondary structure. Much of the region upstream of AAUAAA is sensitive to single-strand-specific nucleases. The region downstream of AAUAAA has both double- and single-stranded characteristics. Both U-rich elements are predominately sensitive to the double-strand-specific nuclease RNase V1, while the G-rich element is primarily single stranded. The U-rich element closest to AAUAAA contains four distinct RNase V1-sensitive regions, which we have designated structural region 1 (SR1), SR2, SR3, and SR4. Linker scanning mutants in the downstream region were analyzed both for structure and for function by in vitro cleavage analyses. These data show that the ability of the downstream region, particularly SR3, to form double-stranded structures correlates with efficient in vitro cleavage. We discuss the possibility that secondary structure downstream of the AAUAAA may be important for the functions of ***polyadenylation*** ***signals*** in general.
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 19 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2000:93982 CAPLUS
DN 132:289464
TI Conserved protein motifs and structural organization of a fish gene homologous to mammalian apolipoprotein E
AU Durliat, Michele; Andre, Michele; Babin, Patrick J.
CS UPRESA 8080 du Centre National de la Recherche Scientifique, Biologie du Developpement des Poissons, Universite Paris-Sud, Orsay, 91405, Fr.
SO European Journal of Biochemistry (2000), 267(2), 549-559 CODEN: EJBCAI; ISSN: 0014-2956
PB Blackwell Science Ltd.
DT Journal
LA English
AB Apolipoprotein E (apoE) plays a central role in lipid metab. from its ability to interact with lipoprotein receptors. Besides its role in cardiovascular diseases, apoE polymorphism contributes to susceptibility to neurodegenerative diseases, such as Alzheimer's disease. The statistical significance of the combined match scores obtained after apoE motif-based protein sequence database ***searches*** , the structural features of the deduced protein, and the phylogenetic anal., support the evidence that a homolog to mammalian apoE can be found in teleost fish. Isolation and characterization of the first nonmammalian APOE revealed that the zebrafish gene spans 2555/2692 bp instead of 3597 bp in human and has the same splice junctions and exon/intron organization as found in mammals, except that there is an addnl. intron that splits the last exon (exon 4) into two exons (exons 4 and 5). Enlargement of APOE size in the mammalian lineage occurs mainly by Alu repeats insertion. The addnl. intron found in zebrafish gene was also identified at the same splicing site in trout APOE and is located in the corresponding linker region following the conserved low d. lipoprotein receptor binding domain. Primer extension and reverse transcriptase PCR (RT-PCR) assays demonstrated that two transcription start sites are located 26 and 28 bp upstream of the first intron and 22 or 24 bp downstream from a canonical TATA box. Sequence inspection of the 5'-flanking region upstream of the TATA box revealed potential regulatory DNA elements. These results will serve as a basis for comparative studies on transcriptional and post-transcriptional mechanisms of APOE regulation in vertebrates.
RE.CNT 58 THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 20 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:805658 CAPLUS
DN 132:262972
TI Developmentally regulated expression of two transcripts for heme oxygenase-2 with a first exon unique to rat testis: control by corticosterone of the oxygenase protein expression
AU Liu, N.; Wang, X.; McCoubrey, W. K.; Maines, M. D.
CS Departments of Biochemistry and Biophysics, University of Rochester School of Medicine, Rochester, NY, USA
SO Gene (2000), 241(1), 175-183 CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.
DT Journal
LA English
AB Heme oxygenase (HO)-2, the constitutive cognate of oxidative stress inducible HO-1 (HSP32), degrades heme to biliverdin, carbon monoxide, and iron. The highest levels of HO-2 are found in the testis. Previously we identified multiple HO-2 homologous transcripts that differ in size and use three different 5' UTRs that form the untranslated first exon of the gene (referred to as rHO-2, rHO-2-1 and rHO-2-2) and two poly(A) signals. Also, we have characterized a functional glucocorticoid response element (GRE) in the promoter region of rHO-2. In this study, we have examd. the structural basis for size heterogeneity of HO-2 transcripts and whether expression of HO-2 at mRNA and protein levels is subject to regulation by corticosterone. Age and tissue-dependence of transcript expression were examd. as well. Our data indicate that the remarkable increase in HO-2 mRNA in adult rat testis is due primarily to generation of two HO-2 homologous transcripts of approx. 2.1 kb and approx. 1.45 kb size that use rHO-2 and are unique to this tissue, and that rHO-2 is not used within other organs. These transcripts are not present in the brain, kidney, thymus, heart, spleen, liver, or in prepubertal 14 day old rat testis. The testis-specific transcripts contain all of the coding region exons present in the approx. 1.3 kb and approx. 1.9 kb transcripts that are common to all organs, including the adult and prepubertal rat testis. Differential use of the poly(A) signals accounts for the difference in size of these two transcripts. Treatment of newborn rats with corticosterone for 5 days, starting on day 2 after birth, induced HO-2 protein expression in the testis as detected by Western blotting. In adult rat testis, corticosterone treatment, however, was not an effective regulator of HO-2 transcript populations or levels. The ***findings*** suggest that HO-2 levels in the testis are controlled by glucocorticoids; and that developmental and tissue-specific factor(s) det. generation of transcripts unique to the organ. The apparent exclusive use of rHO-2 by the mature testis is consistent with the possibility that HO-2 may play a role in male reprodn.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 21 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:804934 CAPLUS
DN 132:118200

TI Genomic structure and transcriptional regulation of the human somatostatin receptor type 2
AU Petersenn, Stephan; Rasch, Anja C.; Presch, Stefanie; Beil, Frank U.; Schulte, Heinrich M.
CS IHF Institute for Hormone and Fertility Research, Department of Medicine, University of Hamburg, Hamburg, 22529, Germany
SO Molecular and Cellular Endocrinology (1999), 157(1-2), 75-85 CODEN: MCEND6; ISSN: 0303-7207
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Somatostatin exerts inhibitory effects on virtually all endocrine and exocrine secretions. The somatostatin receptor subtype 2 (sst2) acts as a crit. mol. for growth hormone regulation and cell proliferation. The authors investigated the structure and regulation of the human sst2 gene. A genomic clone including the sst2 gene was isolated, 1.5 kb of the promoter was sequenced and putative transcription factor binding sites were identified. The transcription start site was located 93 nucleotides upstream of the translation start site. The nucleotide sequences of the complete gene and 0.5 kb of 3' region were detd. A possible ***polyadenylation*** ***signal*** was identified. Transcriptional regulation was investigated by transient transfections using various promoter fragments. A -1100 sst2 promoter directed significant levels of luciferase expression in GH4 rat pituitary cells and Skutl-B endometrium cells whereas only low activity was detected in JEG3 chorion carcinoma cells or COS-7 monkey kidney cells. A minimal -252 promoter allowed cell specific expression. The authors did not ***find*** any regulation of the sst2 promoter by somatostatin, forskolin, TRH, TPA, T3, and 17.beta.-estradiol. Glucocorticoids lead to a significant inhibition of sst2 promoter activity. Further mapping suggest a glucocorticoid- responsive element between - 905 and - 707 and between - 252 and - 163. These studies demonstrate the nature of human sst2 gene and identify its 5' and 3' flanking regions. Furthermore, specific activity of the promoter and regulation by various hormones is demonstrated.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 22 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:555842 CAPLUS
DN 131:347243
TI Occurrence of closely spaced genes in the nuclear genome of the agarophyte Gracilaria gracilis
AU Lluisma, Arturo O.; Ragan, Mark A.
CS Institute for Marine Biosciences, National Research Council of Canada, Halifax, NS, B3H 3Z1, Can.
SO Journal of Applied Phycology (1999), 11(1), 99-104 CODEN: JAPPEL; ISSN: 0921-8971
PB Kluwer Academic Publishers
DT Journal
LA English
AB Little is known about the structure and organization of nuclear genomes in red algae. In particular, it is not known whether genes are densely or loosely packed, whether gene order is conserved, whether their genes tend to occur in one or multiple copies and whether their nuclear genes tend to be compact or interrupted by numerous introns. Sequencing of cloned genomic DNA from Gracilaria gracilis has begun to provide provisional answers to some of these questions. Four pairs of closely spaced genes have been found in G. gracilis upon sequencing genomic clones that contain genes for UDPglucose pyrophosphorylase, galactose-1-phosphate uridylyltransferase, the .beta. subunit of tryptophan synthetase, and methionine sulfoxide reductase (a fifth pair of closely spaced genes, encoding polyubiquitin and aconitase, was reported earlier). An open reading frame with significant similarity to another known gene occurs close (<1.7 kbp) to each of these genes. In two pairs the intergenic region is less than 400 bp in length, and for these the location of the putative ***polyadenylation*** ***signals*** indicates that the gene transcripts, encoded on opposite strands, have overlapping (hence complementary) 3' regions. These somewhat unexpected ***findings*** begin to establish a basis for genome-level characterization of red algae.
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 23 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:503997 CAPLUS
DN 131:270620
TI High expression of a specific T-cell receptor .gamma. transcript in epithelial cells of the prostate
AU Essand, Magnus; Vasmatzis, George; Brinkmann, Ulrich; Duray, Paul; Lee, Byungkook; Pastan, Ira
CS Laboratory of Molecular Biology, Division of Basic Sciences, National Institutes of Health, Bethesda, MD, 20892, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1999), 96(16), 9287-9292 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The authors have identified expression of T-cell receptor .gamma. chain (TCR.gamma.) mRNA in human prostate and have shown that it originates from epithelial cells of the prostate and not from infiltrating T-lymphocytes. In contrast, the T-cell receptor .delta. chain (TCR.delta.) gene is silent in human prostate. The major TCR.gamma. transcript in prostate has a different size than the transcript expressed in thymus, spleen, and blood leukocytes. It is expressed in normal prostate epithelium, adenocarcinoma of the prostate, and the prostatic adenocarcinoma cell line LNCaP. The RNA originates from an unrearranged TCR.gamma. locus, and it is initiated within the intronic sequence directly upstream of the J.gamma.1.2 gene segment. The prostate-specific TCR.gamma. transcript consists of the J.gamma.1.2 and C.gamma.1 gene segments, and it has an untranslated sequence including a ***polyadenylation*** ***signal*** and poly(A) sequence at the 3' end. The ***finding*** that prostate epithelial cells express a high level of a transcript from a gene that was thought to by exclusively expressed by T-lymphocytes is highly unexpected.
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 24 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:486991 CAPLUS
DN 131:238598
TI A novel human GnRH receptor homolog gene: abundant and wide tissue distribution of the antisense transcript
AU Millar, R.; Conklin, D.; Lofton-Day, C.; Hutchinson, E.; Troskie, B.; Illing, N.; Sealfon, S. C.; Hapgood, J.
CS MRC Molecular Reproductive Endocrinology Research Unit, University of Cape Town Medical School, Observatory, 7925, S. Afr.
SO Journal of Endocrinology (1999), 162(1), 117-126 CODEN: JOENAK; ISSN: 0022-0795
PB Society for Endocrinology
DT Journal
LA English
AB Gonadotropin releasing hormone (GnRH) regulates the reproductive system through a specific G-protein-coupled receptor (GPCR) in pituitary gonadotropes. The existence of two (or more) forms of GnRH in most vertebrates suggested the

existence of GnRH receptor subtypes (I and II). Using sequence information for extracellular loop 3 of a putative Type II GnRH receptor from a reptile species, we have looked for a Type II GnRH receptor gene in the human genome EST (expressed sequence tag) database. A homolog was identified which has 45% and 41% amino acid identity with exons 2 and 3 of the known human GnRH pituitary receptor (designated Type I) and much lower homol. with all other GPCRs. A total of 27 contiguous ESTs was found and comprised a continuous sequence of 1642 nucleotides. The EST sequences were confirmed in the cloned human gene and in PCR products of cDNA from several tissues. All EST transcripts detected were in the antisense orientation with respect to the novel GnRH receptor sequence and were highly expressed in a wide range of human brain and peripheral tissues. PCR of cDNA from a wide range of tissues revealed that intronic sequence equiv. to intron 2 of the Type I GnRH receptor was retained. The failure to splice out putative intron sequences in transcripts which spanned exon-intron boundaries is expected in antisense transcripts, as candidate donor and acceptor sites were only present in the gene when transcribed in the orientation encoding the GnRH receptor homolog. No transcripts extended 5' to the sequence corresponding to intron 2 of the Type I GnRH as the antisense transcripts terminated in poly A due to the presence of a ***polyadenylation*** ***signal*** sequence in the putative intron 2 when transcribed in the antisense orientation. These ***findings*** suggest that a Type II GnRH receptor gene has arisen during vertebrate evolution and is also present in the human. However, the receptor may have become vestigial in the human, possibly due to the abundant and universal tissue transcription of the opposite DNA strand to produce antisense RNA.
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 25 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:467621 CAPLUS
DN 131:253157
TI Translocon-associated protein .alpha. transcripts are induced by granulocyte-macrophage colony-stimulating factor and exhibit complex alternative polyadenylation
AU Hirama, Toshiyasu; Miller, Carl W.; Koeffler, H. Phillip
CS Cedars-Sinai Research Institute, Hematology/Oncology Division, UCLA School of Medicine, Los Angeles, CA, USA
SO FEBS Letters (1999), 455(3), 223-227 CODEN: FEBLAL; ISSN: 0014-5793
PB Elsevier Science B.V.
DT Journal
LA English
AB The cloning of full length cDNA for the translocon-assocd. protein .alpha. subunit, previously called signal sequence receptor .alpha., is reported as a result of differential display expts. in ***search*** of genes induced by granulocyte-macrophage colony-stimulating factor. Its mRNA was more abundant in growing cells than in either factor-deprived cells or quiescent cells and comprised four species, each having microheterogeneity, as a result of complex alternative polyadenylation apparently dependent on arrays of non-canonical ***polyadenylation*** ***signals*** . Radiation hybrid mapping of the gene showed that the gene is on the short arm of chromosome 6.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 26 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:404353 CAPLUS
DN 131:180762
TI Utilization of splicing elements and ***polyadenylation*** ***signal*** elements in the coupling of polyadenylation and last-intron removal
AU Cooke, Charles; Hans, Holly; Alwine, James C.
CS Department of Microbiology, School of Medicine, University of Pennsylvania, Philadelphia, PA, 19104-6142, USA
SO Molecular and Cellular Biology (1999), 19(7), 4971-4979 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB Polyadenylation (PA) is the process by which the 3' ends of most mammalian mRNAs are formed. In nature, PA is highly coordinated, or coupled, with splicing. In mammalian systems, the most compelling mechanistic model for coupling arises from data supporting exon definition (2, 34, 37). We have examd. the roles of individual functional components of splicing and PA signals in the coupling process by using an in vitro splicing and PA reaction with a synthetic pre-mRNA substrate contg. an adenovirus splicing cassette and the simian virus 40 late PA signal. The effects of individually mutating splicing elements and PA elements in this substrate were detd. We found that mutation of the polypyrimidine tract and the 3' splice site significantly reduced PA efficiency and that mutation of the AAUAAA and the downstream elements of the PA signal decreased splicing efficiency, suggesting that these elements are the most significant for the coupling of splicing and PA. Although mutation of the upstream elements (USEs) of the PA signal dramatically decreased PA, splicing was only modestly affected, suggesting that USEs modestly affect coupling. Mutation of the 5' splice site in the presence of a viable polypyrimidine tract and the 3' splice site had no effect on PA, suggesting no effect of this element on coupling. However, our data also suggest that a site for U1 snRNP binding (e.g., a 5' splice site) within the last exon can neg. effect both PA and splicing; hence, a 5' splice site-like sequence in this position appears to be a modulator of coupling. In addn., we show that the RNA-protein complex formed to define an exon may inhibit processing if the definition of an adjacent exon fails. This ***finding*** indicates a mechanism for monitoring the appropriate definition of exons and for allowing only pre-mRNAs with successfully defined exons to be processed.
RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 27 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:375093 CAPLUS
DN 131:154434
TI Functional analysis of DNA sequences located within a cluster of DNase I hypersensitive sites colocalizing with a MAR element at the upstream border of the chicken .alpha.-globin gene domain
AU Razin, Sergey V.; Shen, Kang; Ioudinkova, Elena; Scherrer, Klaus
CS Institut J. Monod/Universite Paris 7, Paris, 75251, Fr.
SO Journal of Cellular Biochemistry (1999), 74(1), 38-49 CODEN: JCEBD5; ISSN: 0730-2312
PB Wiley-Liss, Inc.
DT Journal
LA English
AB We have cloned and sequenced a genomic DNA fragment of chicken contg. a cluster of DNase I hypersensitive sites (DHS) located 11-15 kb upstream from the first gene of the .alpha.-globin gene domain and including a constitutive DHS flanked by two erythroid-specific ones. A 1.2-kb subfragment of the DNA fragment under study located upstream to the constitutive DHS and colocalizing roughly with one of the erythroid-specific DHS was shown to possess the properties of a matrix assocn. region

(MAR). The cloned DNA sequences were tested for their ability to serve as promoters and/or influence transcription from the promoter of the .alpha.D globin gene. In the region studied, we did not ***find*** any promoters or enhancers that were active in erythroid cells. The whole DNase I hypersensitive region and some of its subfragments showed a silencing effect when placed downstream from the reporter gene. The expression of the reporter gene was completely abolished, however, when these DNA fragments were placed between the .alpha.D promoter and the reporter gene. Thus, they seem to act as transcription "terminators.". Numerous ***polyadenylation*** ***signals*** (AATAAA) and an AT-rich palindrome were found within the sequenced DNA fragment. These observations are discussed within the frame of the hypothesis postulating that continuous transcription is essential for maintaining the active status of genomic domains. Furthermore, it is suggested that the DNA fragment studied contains a neg. control element that keeps globin genes silent within the chromatin domain permanently open in nonerythroid cells.
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 28 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:283849 CAPLUS
DN 131:112200
TI Cloning and characterization of mtDBP, a DNA-binding protein which binds two distinct regions of sea urchin mitochondrial DNA
AU Polosa, Paola Loguercio; Roberti, Marina; Musicco, Clara; Gadaleta, Maria Nicola; Quagliariello, Ernesto; Cantatore, Palmiro
CS Dipartimento di Biochimica e Biologia Molecolare, Universita di Bari and the Centro Studi sui Mitocondri e Metabolismo Energetico CNR, Bari, 70125, Italy
SO Nucleic Acids Research (1999), 27(8), 1890-1899 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The cDNA for the sea urchin mitochondrial D-loop-binding protein (mtDBP), a 40 kDa protein which binds two homologous regions of mitochondrial DNA (the D-loop region and the boundary between the oppositely transcribed ND5 and ND6 genes), has been cloned. Four different 3'-untranslated regions have been detected that are related to each other in pairs and do not contain the canonical ***polyadenylation*** ***signal*** . The in vitro synthesized mature protein (348 amino acids), deprived of the putative signal sequence, binds specifically to its DNA target sequence and produces a DNase I footprint identical to that given by the natural protein. MtDBP contains two leucine zippers, one of which is bipartite, and two small N- and C-terminal basic domains. A deletion mutation anal. of the recombinant protein has shown that the N-terminal region and the two leucine zippers are necessary for the binding. Furthermore, evidence was provided that mtDBP binds DNA as a monomer. This rules out a dimerization role for the leucine zippers and rather suggests that intramol. interactions between leucine zippers take place. A database ***search*** has revealed as the most significative homol. a match with the human mitochondrial transcription termination factor (mTERF), a protein that also binds DNA as a monomer and contains three leucine zippers forming intramol. interactions. These similarities, and the observation that mtDBP-binding sites contain the 3'-ends of mtRNAs coded by opposite strands and the 3'-end of the D-loop structure, point to a dual function of the protein in modulating sea urchin mitochondrial DNA transcription and replication.
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 29 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:268720 CAPLUS
DN 131:112173
TI Characterization of the Gene Encoding Human TAFI (Thrombin-Activable Fibrinolysis Inhibitor; Plasma Procarboxypeptidase B)
AU Boffa, Michael B.; Reid, T. Scott; Joo, Emily; Nesheim, Michael E.; Koschinsky, Marlys L.
CS Departments of Biochemistry and Medicine, Queen's University, Kingston, ON, K7L 3N6, Can.
SO Biochemistry (1999), 38(20), 6547-6558 CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
AB Thrombin-activable fibrinolysis inhibitor (TAFI) is a recently described human plasma zymogen that is related to pancreatic carboxypeptidase B. The active form of TAFI (TAFIa), which is formed by thrombin cleavage of the zymogen, likely inhibits fibrinolysis by removal from partially degraded fibrin of the carboxyl-terminal lysine residues which act to stimulate plasminogen activation. The authors have isolated and characterized genomic clones which encompass the entire human TAFI gene from .lambda. phage and bacterial artificial chromosome genomic libraries. The complete TAFI gene contains 11 exons and spans approx. 48 kb of genomic DNA. The positions of intron/exon boundaries are conserved between the TAFI gene and the rat pancreatic carboxypeptidase A1, A2, and B and the human mast cell carboxypeptidase A genes, indicating that these carboxypeptidases arose from a common ancestral gene. However, the intron lengths diverge significantly among all of these genes. The TAFI promoter lacks a consensus TATA sequence, and transcription is initiated from multiple sites. Transient transfection of reporter plasmids contg. portions of the TAFI 5'-flanking region into mammalian cells allowed localization of the promoter and identified a .apprx.70 bp region crucial for liver-specific transcription. Sequence anal. of cDNA clones obtained from human liver RNA indicated that the TAFI transcript is polyadenylated at three different sites. The authors' ***findings*** will facilitate the assessment of the regulation of TAFI expression by transcriptional and/or posttranscriptional mechanisms. Furthermore, knowledge of the genomic structure of the TAFI gene will aid in the identification of mutations that may be assocd. with the tendency to either bleed or thrombose.
RE.CNT 64 THERE ARE 64 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 30 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:263458 CAPLUS
DN 131:71024
TI The C-terminal region but not the Arg-X-Pro repeat of Epstein-Barr virus protein EB2 is required for its effect on RNA splicing and transport
AU Buisson, Monique; Hans, Fabienne; Kusters, Inca; Duran, Nathalie; Sergeant, Alain
CS U412 INSERM, Ecole Normale Supnrieure de Lyon, Lyon, 69364, Fr.
SO Journal of Virology (1999), 73(5), 4090-4100 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB The Epstein-Barr virus BMLF1 gene product EB2 has been shown to efficiently transform immortalized Rat1 and NIH 3T3 cells, to bind RNA, and to shuttle from the nucleus to the cytoplasm. In transient-expression assays EB2 seems to affect

mRNA nuclear export of intronless RNAs and pre-mRNA 3' processing, but no direct proof of EB2 being involved in RNA processing and transport has been provided, and no specific functional domain of EB2 has been mapped. Here we significantly extend these ***findings*** and directly demonstrate that (i) EB2 inhibits the cytoplasmic accumulation of mRNAs, but only if they are generated from precursors contg. weak (cryptic) 5' splice sites, (ii) EB2 has no effect on the cytoplasmic accumulation of mRNA generated from precursors contg. constitutive splice sites, and (iii) EB2 has no effect on the 3' processing of precursor RNAs contg. canonical and noncanonical cleavage- ***polyadenylation*** ***signals*** . We also show that in the presence of EB2, intron-contg. and intronless RNAs accumulate in the cytoplasm. EB2 contains an Arg-X-Pro tripeptide repeated eight times, similar to that described as an RNA-binding domain in the herpes simplex virus type 1 protein USI1. As glutathione S-transferase fusion proteins, both EB2 and the Arg-X-Pro repeat bound RNA in vitro. However, by using EB2 deletion mutants, we demonstrated that the effect of EB2 on splicing and RNA transport requires the C-terminal half of the protein but not the Arg-X-Pro repeat.
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 31 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:250626 CAPLUS
DN 131:69056
TI Nucleotide structure and characterization of the murine gene encoding the endothelial cell protein C receptor
AU Liang, Zhong; Rosen, Elliot D.; Castellino, Francis J.
CS Department Chemistry Biochemistry, University Notre Dame, Notre Dame, IN, 46556, USA
SO Thrombosis and Haemostasis (1999), 81(4), 585-588 CODEN: THHADQ; ISSN: 0340-6245
PB F. K. Schattauer Verlagsgesellschaft mbH
DT Journal
LA English
AB The nucleotide sequence of the entire gene encoding the murine endothelial cell receptor for activated protein C (EPCR) was detd. A total of 5303 bp of DNA was sequenced that included 4 exons and 3 introns, which constituted the coding region of the gene, as well as 393 bp upstream of the first exon and 841 bp downstream of the last exon. From the locations of the introns in this gene and anal. of the exon structures, it is clear the EPCR gene is a member of the CD1 class of multiple histocompatibility proteins, and its cDNA sequence is nearly identical to that of CCD41, a centrosome-assocd. protein. All elements needed for RNA polymerase II-based transcription are predicted to exist in the 5' uncoded region of the gene, and potential 3' regulatory sequences for efficient polyadenylation were located at their optimal locations. A variety of highly probable transcription factor binding sites were located in the 5' region of the gene. These data suggest that the EPCR gene is under efficient transcriptional control, and support the ***finding*** that this gene product may be involved in the inflammatory pathway.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 32 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:244123 CAPLUS
DN 131:83890
TI Nonsense mutations in the alcohol dehydrogenase gene of Drosophila melanogaster correlate with an abnormal 3' end processing of the corresponding pre-mRNA
AU Brogna, Saverio
CS Department of Genetics, University of Cambridge, Cambridge, CB2 3EH, UK
SO RNA (1999), 5(4), 562-573 CODEN: RNARFU; ISSN: 1355-8382
PB Cambridge University Press
DT Journal
LA English
AB From bacteria to mammals, mutations that generate premature termination codons have been shown to result in the redn. in the abundance of the corresponding mRNA. In mammalian cells, more often than not, the redn. happens while the RNA is still assocd. with the nucleus. Here, it is reported that mutations in the alc. dehydrogenase gene (Adh) of Drosophila melanogaster that generate premature termination codons lead to reduced levels of cytoplasmic and nuclear mRNA. Unexpectedly, it has been found that the poly(A) tails of Adh mRNAs and pre-mRNAs that carry a premature termination codon are longer than in the wild-type transcript. The more 5' terminal the mutation is, the longer is the poly(A) tail of the transcript. These ***findings*** suggest that the integrity of the coding region may be required for accurate mRNA 3' end processing.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 33 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:68836 CAPLUS
DN 130:247722
TI Cloning and phylogenetic relationship of red drum somatolactin cDNA and effects of light on pituitary somatolactin mRNA expression
AU Zhu, Yong; Yoshiura, Yasutoshi; Kikuchi, Kiyoshi; Aida, Katsumi; Thomas, Peter
CS Marine Science Institute, University of Texas at Austin, Port Aransas, TX, 78373, USA
SO General and Comparative Endocrinology (1999), 113(1), 69-79 CODEN: GCENA5; ISSN: 0016-6480
PB Academic Press
DT Journal
LA English
AB The nucleotide sequence for red drum somatolactin (SL) cDNA was detd. and the expression of pituitary SL mRNA was examd. in red drum kept under various light conditions. A full length of SL cDNA (1629 bp) was isolated and characterized from a red drum pituitary cDNA library. The SL cDNA has an open reading frame of 696 nucleotides which encodes a 24-amino-acid signal peptide and a 207-amino-acid mature peptide. Red drum SL shares 58-87% amino acid sequence identity and 56-85% nucleotide sequence identity with other teleost SLs. The characteristic seven cysteine residues and one N-glycosylation site of SL are well conserved in the red drum SL mature peptide. Phylogenetic anal. shows that red drum SL is closely related to seabream SL and is also closely related to lumpfish, flounder, halibut, and sole SLs, whereas SLs of Atlantic cod, chum salmon, rainbow trout, and eel are more distantly related to those of the more advanced teleosts. Two SL transcripts, designated as SL I at 1.8 kb and SL II at 1.3 kb, are expressed in red drum pituitaries and correspond to two ***polyadenylation*** ***signal*** sites in red drum SL cDNA at nucleotide positions 1554 and 1270. Levels of the SL I mRNA were 2- to 4-fold higher in pituitaries of blind red drum and intact fish kept under const. darkness for 1 wk than those in control fish sampled during the light phase of the light-dark cycle. Similarly, pituitary levels of SL II mRNA were 9-fold higher in blind fish and 1.6- to 4-fold higher in intact fish kept under const. darkness than in the control fish. Furthermore, these changes in mRNA levels in pituitaries were accompanied by more than 10-fold increases in SL protein concns. in plasma. The ***finding*** that the absence of light perception for extended periods leads to dramatic increases in SL mRNA expression as well as SL secretion in red drum provides

further evidence that illumination levels and SL physiol. are intimately related in this species. (c) 1999 Academic Press.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 34 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:20845 CAPLUS
DN 130:192448
TI Homology-based gene prediction using neural nets
AU Cai, Yudong; Bork, Peer
CS EMBL, Heidelberg, 690 12, Germany
SO Analytical Biochemistry (1998), 265(2), 269-274 CODEN: ANBCA2; ISSN: 0003-2697
PB Academic Press
DT Journal
LA English
AB We have developed and implemented a method for computational gene identification called GIN (gene identification using neural nets and homol. information) that has been particularly designed to avoid false pos. predictions. It thus predicts 55% of all genes tested correctly, has a specificity of 99%, but also has an overall accuracy of 92% on a benchmark set of 570 vertebrate genes constructed by Burset and Guigo. The method combines homol. ***searches*** in protein and expressed sequence tag databases with several neural networks designed to recognize start codons, Poly(A) signals, stop codons, and splice sites. Predicted exons are assembled into genes using a homol.-based scoring function. GIN is able to recognize multiple genes within genomic DNA as demonstrated by the identification of a globin gene (.gamma.-globin-1 (G)) that has not been annotated as a coding region in the widely used the test set of Burset and Guigo. Furthermore, GIN identifies more than 107 other protein hits in noncoding regions and classifies them into possible pseudogenes or splice variants. (c) 1998 Academic Press.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 35 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:810720 CAPLUS
DN 130:163891
TI Model for polymerase access to the overlapped L gene of respiratory syncytial virus
AU Fearns, Rachel; Collins, Peter L.
CS Laboratory of Infectious Diseases, National Institute of Allergy and Infectious Diseases, Bethesda, MD, 20892-0720, USA
SO Journal of Virology (1999), 73(1), 388-397 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB The last two genes of respiratory syncytial virus (RSV), M2 and L, overlap by 68 nucleotides, an arrangement which has counterparts in a no. of nonsegmented neg.-strand RNA viruses. Thus, the gene-end (GE) signal of M2 lies downstream of the L gene-start (GS) signal, sepd. by 45 nucleotides. Since RSV transcription ostensibly is sequential and unidirectional from a single promoter within the 3' leader region, it was unclear how the polymerase accesses the L GS signal. Furthermore, it was previously shown that 90% of transcripts which are initiated at the L GS ***signal*** are ***polyadenylated*** and terminated at the M2 GE signal, yielding a short, truncated L mRNA as the major transcription product of the L gene. Despite these apparent down-regulatory features, we show that the accumulation of full-length L mRNA during RSV infection is only sixfold less than that of its upstream neighbor, M2. We used cDNA-encoded genome analogs in an intracellular transcription assay to investigate the mechanism of transcription of the overlapped genes. Expression of L was found to be dependent on sequential transcription from the 3' end of the genome. Apart from the L GS signal, the only other strict requirement for initiation at L was the M2 GE signal. This implies that the polymerase accesses the L GS signal only following arrival at the M2 GE signal. Thus, polymerase which terminates at the M2 GE signal presumably scans upstream to initiate at the L GS signal. This also would provide a mechanism whereby polymerase which terminates prematurely during transcription of L could recycle from the M2 GE signal to the L GS signal, thereby accounting for the unexpectedly high level of synthesis of full-length L mRNA. The sequence and spacing between the two signals were not crit. Furthermore, the polymerase also was capable of efficiently transcribing from an L GS signal placed downstream of the M2 GE signal, implying that the overlapping arrangement is not obligatory. When copies of the L GS signal were placed concurrently upstream and downstream of the M2 GE signal, both were utilized. This ***finding*** indicates that a polymerase situated at a GE signal is capable of scanning for a GS signal in either the upstream or downstream direction and thereafter initiating transcription.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 36 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:810688 CAPLUS
DN 130:178233
TI Genetic dissociation of the encapsidation and reverse transcription functions in the 5' R region of human immunodeficiency virus type 1
AU Clever, Jared L.; Eckstein, Daniel A.; Parslow, Tristram G.
CS Departments of Pathology and of Microbiology and Immunology, University of California, San Francisco, CA, 94143, USA
SO Journal of Virology (1999), 73(1), 101-109 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB The efficient packaging of genomic RNA into virions of human immunodeficiency virus type 1 (HIV-1) is directed by cis-acting encapsidation signals, which have been mapped to particular RNA stem-loop structures near the 5' end of the genome. Earlier studies have shown that three such stem-loops, located adjacent to the major 5' splice donor, are required for optimal packaging; more recent reports further suggest a requirement for the TAR and poly(A) hairpins of the 5' R region. In the present study, we have compared the phenotypes that result from mutating these latter elements in the HIV-1 provirus. Using a single-round infectivity assay, we ***find*** that mutations which disrupt base pairing in either the TAR or poly(A) stems cause profound defects in both packaging and viral replication. Decreased genomic packaging in a given mutant was always accompanied by increased packaging of spliced viral RNAs. Compensatory mutations that restored base pairing also restored encapsidation, indicating that the secondary structures of the TAR and poly(A) stems, rather than their primary sequences, are important for packaging activity. Despite having normal RNA contents, however, viruses with compensatory mutations at the base of the TAR stem were severely replication defective, owing to a defect in proviral DNA synthesis. Our ***findings*** thus confirm that the HIV-1 TAR stem-loop is required for at least three essential viral functions (transcriptional activation, RNA packaging, and reverse transcription) and reveal that its packaging and reverse transcription activities can be dissocd. genetically by mutations at the base of the TAR stem.

RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 37 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:736719 CAPLUS
DN 130:77554
TI Poly(A)-tail-promoted translation in yeast: implications for translational control
AU Preiss, Thomas; Muckenthaler, Martina; Hentze, Matthias W.
CS Gene Expression Programme, European Molecular Biology Laboratory, Heidelberg, D-69117, Germany
SO RNA (1998), 4(11), 1321-1331 CODEN: RNARFU; ISSN: 1355-8382
PB Cambridge University Press
DT Journal
LA English
AB The cap structure and the poly(A) tail synergistically activate mRNA translation in vivo. Recent work using Saccharomyces cerevisiae spheroplasts and a yeast cell-free translation system revealed that the poly(A) tail can function as an independent promoter for ribosome recruitment, to internal initiation sites within an mRNA. This raises the question of how regulatory upstream open reading frames and translational repressor proteins binding to the 5' UTR can function, as well as how regulated polyadenylation can support faithful activation of protein synthesis. We investigated the function of the regulatory upstream open reading frame 4 from the yeast GCN 4 gene and the effect of IRP-1 binding to an iron-responsive element introduced into the 5' UTR of reporter mRNAs. Both manipulations effectively block cap-dependent translation, whereas ribosome recruitment promoted by the poly(A) tail under non-competitive conditions can efficiently bypass both blocks. We show that the synergistic use of both, the cap structure and the poly-A tail enforced by mRNA competition reinstates the full extent of translational control by both types of 5' UTR regulatory elements. With a view towards regulated polyadenylation, we studied the function of poly(A) tails of defined length on the translation of capped mRNAs. We ***find*** that poly(A) tail elongation increases translational efficiency, particularly under competitive conditions. Our results integrate recent ***findings*** on the function of the poly(A) tail into an understanding of translational control.
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 38 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:701477 CAPLUS
DN 130:50617
TI A pilot study testing the association between N-acetyltransferases 1 and 2 and risk of oral squamous cell carcinoma in Japanese people
AU Katoh, Takahiko; Kaneko, Shigeru; Boissy, Robert; Watson, Mary; Ikemura, Kunio; Bell, Douglas A.
CS National Institute of Environmental Health Sciences, NC, 27709, USA
SO Carcinogenesis (1998), 19(10), 1803-1807 CODEN: CRNGDP; ISSN: 0143-3334
PB Oxford University Press
DT Journal
LA English
AB Risk of oral cancer has been assocd. with exposure to tobacco smoke, alc. and with genetic predisposition. The arom. amines and their metabolites, a class of carcinogens present in tobacco smoke, undergo metab. (activation or detoxification) through an N- or O-acetylation pathway by the polymorphic enzymes, N-acetyltransferases (NAT)1 or NAT2. The genes that encode these enzymes, NAT1 and NAT2, have a variety of high and low activity alleles and we analyzed these genetic polymorphisms in 62 oral squamous cell carcinoma cases, and 122 healthy control subjects from Japan. NAT1 alleles tested were NAT1*3 (C1095A), NAT1*4 (functional ref. allele), NAT1*10 (T1088A,C1095A), NAT1*11(9 bp deletion), NAT1*14 (G560A), NAT1*15 (C559T) and NAT1*17 (C190T). No low activity alleles (NAT1*14, NAT1*15 and NAT1*17) were obsd. in these Japanese subjects. We obsd. significantly increased risk assocd. with the NAT1*10 allele, an allele that contains a variant ***polyadenylation*** ***signal*** . Stratifying by smoking status we found odds ratios of 5.9 for non-smokers with the NAT1*10 allele and 3.1 for smokers, but these risks were not significantly different from each other. Thus, we did not observe that NAT1*10 alleles confer differential risk among smokers and non-smokers. NAT2 rapid acetylation genotype was not a significant risk factor for oral cancer in this Japanese study population. This is the first study to test for oral cancer risk assocd. with polymorphism in the NAT1 and NAT2 genes, and these pos. ***findings*** in our pilot study, while based on small nos., suggest that the NAT1*10 allele may be a genetic determinant of oral squamous cell carcinoma among Japanese people.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 39 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:694318 CAPLUS
DN 130:61852
TI Genomic organization of four .beta.-1,4-endoglucanase genes in plant-parasitic cyst nematodes and its evolutionary implications
AU Yan, Yitang; Smant, Geert; Stokkermans, Jack; Qin, Ling; Helder, Johannes; Baum, Thomas; Schots, Arjen; Davis, Eric
CS Plant Pathology Department, North Carolina State University, Raleigh, NC, 27695, USA
SO Gene (1998), 220(1-2), 61-70 CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.
DT Journal
LA English
AB The genomic organization of genes encoding .beta.-1,4-endoglucanases (cellulases) from the plant-parasitic cyst nematodes Heterodera glycines and Globodera rostochiensis (HG-eng1, Hg-eng2, GR-eng1, and GR-eng2) was investigated. HG-eng1 and GR-eng1 both contained eight introns and structural domains of 2151 and 2492 bp, resp. HG-eng2 and GR-eng2 both contained seven introns and structural domains of 2324 and 2388 bp, resp. No significant similarity in intron sequence or size was obsd. between HG-eng1 and HG-eng2, whereas the opposite was true between GR-eng1 and GR-eng2. Intron positions among all four cyst nematode cellulase genes were conserved identically in relation to the predicted amino acid sequence. HG-eng1, GR-eng1, and GR-eng2 had several introns demarcated by 5'-GC...AG-3' in the splice sites, and all four nematode cellulase genes had the ***polyadenylation*** and cleavage ***signal*** sequence 5'-GAUAAA-3'-both rare occurrences in eukaryotic genes. The 5'-flanking regions of each nematode cellulase gene, however, had signature sequences typical of eukaryotic promoter regions, including a TATA box, bHLH-type binding sites, and putative silencer, repressor, and enhancer elements. Database ***searches*** and subsequent phylogenetic comparison of the catalytic domain of the nematode cellulases placed the nematode genes in one group, with Family 5, subfamily 2, glycosyl hydrolases from Scotobacteria and Bacillaceae as the most homologous groups. The overall amino acid sequence identity among the four nematode cellulases was from 71 to 83%, and the amino acid sequence identity to bacterial Family 5 cellulases ranged from 33 to 44%. The eukaryotic organization of the four cyst nematode cellulases suggests that they share a common

ancestor, and their strong homol. to prokaryotic glycosyl hydrolases may be indicative of an ancient horizontal gene transfer.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 40 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:397203 CAPLUS
DN 129:145498
TI Human rab11a: transcription, chromosome mapping and effect on the expression levels of host GTP-binding proteins
AU Gromov, Pavel S.; Celis, Julio E.; Hansen, Claus; Tommerup, Niels; Gromova, Irina; Madsen, Peder
CS Department of Medical Biochemistry and Danish Centre for Human Genome Research, Aarhus University, Aarhus, DK-8000, Den.
SO FEBS Letters (1998), 429(3), 359-364 CODEN: FEBLAL; ISSN: 0014-5793
PB Elsevier Science B.V.
DT Journal
LA English
AB Rab11a is a member of the rab-branch of the ras-like small GTP-binding protein superfamily that is assocd. with both constitutive and regulated secretory pathways. Using a direct procedure for cDNA cloning of small ras-related GTPases, that is based on the screening of eukaryotic cDNA expression libraries using [.alpha.-32P]GTP as a probe, we have isolated two cDNA clones encoding rab11a. Both clones share identical coding sequences, but differ in the length and sequence of their 3' untranslated regions (3'-UTR). Northern blot hybridization anal. of various human tissues revealed indeed two mRNA species with lengths of 1.0 and 2.3 kb, resp. Sequence anal. of the cDNAs identified two different putative ***polyadenylation*** ***signals*** (AATAAA) at positions 927 and 2302 of the larger transcript. In addn., the 3'-UTR of the larger transcript exhibited several AU-rich elements (ARE) that are believed to control gene expression by regulating the rate of mRNA degrdn. Southern blots of human DNA digested with several rare restriction enzymes, and sepd. by pulse-field gel electrophoresis, yielded the same macro-restriction fragment pattern when hybridized with probes that discriminate between the two transcripts. Taken together, these ***findings*** imply that the two mRNA species originate from a single gene, which we have mapped to 15q21.3-q22.31, by the use of different polyadenylation sites. As expected, both rab11a-cDNAs yielded the same protein product when transiently expressed in COS-1 cells, and surprisingly, upregulated the proteome expression profile (de novo synthesis or posttranslational modification of preexisting proteins) of a few other, yet unknown GTP-binding proteins.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 41 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:395595 CAPLUS
DN 129:132098
TI Transcription of hepatitis delta antigen mRNA continues throughout hepatitis delta virus (HDV) replication: a new model of HDV RNA transcription and replication
AU Modahl, Lucy E.; Lai, Michael M. C.
CS Department of Molecular Microbiology and Immunology, University of Southern California School of Medicine, Los Angeles, CA, 90033-1054, USA
SO Journal of Virology (1998), 72(7), 5449-5456 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB Hepatitis delta virus (HDV) replicates by RNA-dependent RNA synthesis according to a double rolling circle model. Also synthesized during replication is a 0.8-kb, polyadenylated mRNA encoding the hepatitis delta antigen (HDAg). It has been proposed that this mRNA species represents the initial product of HDV RNA replication; subsequent prodn. of genomic-length HDV RNA relies on suppression of the HDV RNA ***polyadenylation*** ***signal*** by HDAg. However, this model was based on studies which required the use of an HDV cDNA copy to initiate HDV RNA replication in cell culture, thus introducing an artificial requirement for DNA-dependent RNA synthesis. We have now used an HDV cDNA-free RNA transfection system and a method that we developed to detect specifically the mRNA species transcribed from the HDV RNA template. We established that this polyadenylated mRNA is 0.8 kb in length and its 5' end begins at nucleotide 1631. Suprisingly, kinetic studies showed that this mRNA continued to be synthesized even late in the viral replication cycle and that the mRNA and the genomic-length RNA increased in parallel, even in the presence of HDAg. Thus, a switch from prodn. of the HDAg mRNA to the full-length HDV RNA does not occur in this system, and suppression of the polyadenylation site by HDAg may not significantly regulate the synthesis of the HDAg mRNA, as previously proposed. These ***findings*** reveal novel insights into the mechanism of HDV RNA replication. A new model of HDV RNA replication and transcription is proposed.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 42 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:343902 CAPLUS
DN 129:105043
TI Characterization of the gene encoding the human Kidd blood group/urea transporter protein. Evidence for splice spite mutations in Jknull individuals
AU Lucien, Nicole; Sidoux-Walter, Frederic; Olives, Bernadette; Moulds, Joann; Le Pennec, Pierre-Yves; Cartron, Jean-Pierre; Bailly, Pascal
CS Inst. National Transfusion Sanguine, Paris, 75015, Fr.
SO Journal of Biological Chemistry (1998), 273(21), 12973-12980 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB The Kidd (JK) blood group is carried by an integral membrane glycoprotein which transports urea through the red cell membrane and is also present on endothelial cells of the vasa recta in the kidney. The exon-intron structure of the human blood group Kidd/urea transporter gene has been detd. It is organized into 11 exons distributed over 30 kilobase pairs. The mature protein is encoded by exons 4-11. The transcription initiation site was identified by 5'-rapid amplification of cDNA ends-polymerase chain reaction at 335 base pairs upstream of the translation start point located in exon 4. The 5'-flanking region, from nucleotide -837 to -336, contains TATA and inverted CAAT boxes as well as GATA-1/SP1 erythroid-specific cis-acting regulatory elements. Anal. of the 3'-untranslated region reveals that the two equally abundant erythroid transcripts of 4.4 and 2.0 kilobase pairs arise from usage of different alternative ***polyadenylation*** ***signals*** . No obvious abnormality of the Kidd/urea transporter gene, including the 5'- and 3'-untranslated regions, has been detected by Southern blot anal. of the blood of two unrelated Jknull individuals (B.S. and L.P.), which lacks all Jk antigens and Jk proteins on red cells, but was genotyped as homozygous for a "silent" Jkb allele. Further anal. indicated that different splice site mutations occurred in each variant. The first mutation affected the invariant G residue of the

3'-acceptor splice site of intron 5 (variant B.S.), while the second mutation affected the invariant G residue of the 5'-donor splice site of intron 7 (variant L.P.). These mutations caused the skipping of exon 6 and 7, resp., as seen by sequence anal. of the Jk transcripts present in reticulocytes. Expression studies in Xenopus oocytes demonstrated that the truncated proteins encoded by the spliced transcripts did not mediate a facilitated urea transport compared with the wild type Kidd/urea transporter protein and were not expressed on the oocyte's plasma membrane. These ***findings*** provide a rational explanation for the lack of Kidd/urea transporter protein and defect in urea transport of Jknull cells.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 43 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:342866 CAPLUS
DN 129:91253
TI Statistical features of human exons and their flanking regions
AU Zhang, M. Q.
CS Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 11724, USA
SO Human Molecular Genetics (1998), 7(5), 919-932 CODEN: HMGEE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
AB To facilitate gene ***finding*** and for the investigation of human mol. genetics on a genome scale, the author presents a comprehensive survey on various statistical features of human exons. The author first shows that human exons with flanking genomic DNA sequences can be classified into 12 mutually exclusive categories. This classification could serve as a std. for future studies so that direct comparisons of results can be made. A database for eight categories (related to human genes in which coding regions are split by introns) was built from GenBank release 87.0 and analyzed by a no. of methods to characterize statistical features of these sequences that may serve as controls or regulatory signals for gene expression. The statistical information compiled includes profiles of signals for transcription, splicing and translation, various compositional statistics and size distributions. Further analyses reveal novel correlations and constraints among different splicing features across an internal exon that are consistent with the Exon Definition model. This information is fundamental for a quant. view of human gene organization, and should be invaluable for individual scientists to design human mol. genetics expts.
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 44 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:297699 CAPLUS
DN 129:52412
TI Expression of SRY gene transcripts with a longer 3' untranslated sequence in adult human male lymphocytes and tumor cells
AU Kimoto, Y.
CS Department of Surgical Oncology, Biomedical Research Center, Osaka University Medical School, Suita, 565, Japan
SO Molecular & General Genetics (1998), 257(5), 587-593 CODEN: MGGEAE; ISSN: 0026-8925
PB Springer-Verlag
DT Journal
LA English
AB Using 3' RACE PCR and the repeated nested-PCR method, the expression of transcripts of the sex-detg. gene SRY was investigated in single lymphocytes from a human adult male and in male tumor cell lines. The gene is functionally transcribed in the early stages of embryogenesis and mRNA is also expressed in adult testes. However, in this study, SRY gene transcripts were also detected in somatic cells of adult male and in tumor cells. Moreover, this mRNA possessed a longer addnl. untranslated exon. Although expression of the transcripts might not have any functional meaning in these cells, these new ***findings*** support the hypothesis that any given human cell can contain illegitimate mRNAs.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 45 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:243588 CAPLUS
DN 129:36996
TI ES2, a gene deleted in DiGeorge syndrome, encodes a nuclear protein and is expressed during early mouse development, where it shares an expression domain with a Goosecoid-like gene
AU Lindsay, Elizabeth A.; Harvey, Emma L.; Scambler, Peter J.; Baldini, Antonio
CS Department of Mol. and Human Genetics, Baylor College of Medicine, Houston, TX, 77030, USA
SO Human Molecular Genetics (1998), 7(4), 629-635 CODEN: HMGEE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
AB ES2 is a gene deleted in DiGeorge syndrome (DGS) and velocardiofacial syndrome (VCFS) which has homologs in species as distant as Caenorhabditis elegans and Drosophila. The function of ES2 is unknown, and the predicted protein sequence does not contain motifs which suggest a particular role in the development defects present in DGS and VCFS. Here we show that the mouse homolog, ES2, is transcribed in two forms resulting from the use of alternative ***polyadenylation*** ***signals*** . Structural anal. programs predict that the Es2-encoded peptide has a coiled-coil domain, and transfection expts. with an Es2-green fluorescent protein (GFP) fusion construct show that the peptide is recruited into the nucleus. Es2 is highly expressed during mouse embryogenesis from E7 onwards. In situ hybridization with an RNA probe revealed that the gene is widely expressed; however, relatively higher expression was detected in the nervous system, with a particularly high area of expression in a sub-region of the pons. The Es2 expression domain in the pons is shared with a Goosecoid-like gene (Gscl) which is located upstream of ES2, and raises the possibility that the two genes share regulatory elements an/or interact in this region of the developing brain. This ***finding*** suggests that different genes in the deleted region may be functionally related and might explain the occurrence of the characteristic phenotype in patients with non-overlapping genetic lesions.
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 46 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:73018 CAPLUS
DN 129:13026
TI Organization, 5'-flanking sequence and promoter activity of the rat GPC1 gene
AU Asundi, Vinod K.; Keister, Bonnie F.; Carey, David J.
CS Penn State University College of Medicine, Janet Weis Center for Research, Sigfried, Research Program, MD, Henry Hood, Pennsylvania State University, 100 North Academy Avenue, Danville, PA, 17822, USA
SO Gene (1998), 206(2), 255-261 CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.

DT Journal
LA English
AB Glypicans are a member of a family of glycosylphosphatidylinositol anchored heparan sulfate proteoglycans that are expressed in cell and development specific patterns. Rat GPC1 cDNA probes were used to screen rat genomic libraries. Three overlapping genomic clones that contained the entire rat GPC1 gene were isolated. The rat GPC1 gene is approx. 15 kb in length and consists of eight exons interrupted by introns of varying lengths. Two of the introns are quite short, with lengths of 41 and 43 base pairs. Each exon-intron splice junction exhibited the consensus splice site sequence. Exon 1 encodes the putative signal peptide and the serine residue of the first putative heparan sulfate attachment site. The last exon encodes the cluster of three potential COOH-terminal heparan sulfate attachment sites, the putative GPI anchor and polypeptide cleavage site, and the 3'-untranslated region including the ***polyadenylation*** ***signal*** . One of the genomic clones extended approx. 2.8 kb 5' of the exon 1 coding sequence, and is thus likely to contain sequences that regulate GPC1 gene expression. Sequence anal. of the 5'-flanking sequence revealed a lack of consensus TATA and CAAT boxes. A ***search*** for potential transcription factor binding sites revealed a no. of such motifs, including Sp1 (GC box), NF-.kappa.B, and MyoD (E-box). This region of the rat GPC1 gene shows significant sequence homol. to the 5'-flanking region of the human GPC3 gene. Functional promoter activity of the rat GPC1 sequence was demonstrated by its ability to drive the expression of a luciferase reporter gene in several cell types.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 47 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:30668 CAPLUS
DN 128:176697
TI Structure of the mouse leukemia inhibitory factor receptor gene: regulated expression of mRNA encoding a soluble receptor isoform from an alternative 5' untranslated region
AU Chambers, Ian; Cozens, Alison; Broadbent, Joanne; Robertson, Morag; Lee, Muriel; Li, Meng; Smith, Austin
CS Centre for Genome Research, University of Edinburgh, Edinburgh, EH9 3JO, UK
SO Biochemical Journal (1997), 328(3), 879-888 CODEN: BIJOAK; ISSN: 0264-6021
PB Portland Press Ltd.
DT Journal
LA English
AB The low-affinity leukemia inhibitory factor receptor (LIF-R) is a component of cell-surface receptor complexes for the multi-functional cytokines leukemia inhibitory factor, ciliary neurotrophic factor, oncostatin M and cardiotrophin-1. Both sol. and transmembrane forms of the protein have been described and several LIF-R mRNAs have been reported previously. In order to det. the coding potential of LIF-R mRNAs we have isolated and characterized the mouse LIF-R gene. MRNA encoding sol. LIF-R (sLIF-R) is formed by inclusion of an exon in which ***polyadenylation*** ***signals*** are provided by a B2 repeat. This exon is located centrally within the LIF-R gene but is excluded from the transmembrane LIF-R mRNA by alternative splicing. The transmembrane receptor is encoded by 19 exons distributed over 38 kb. Two distinct 5' non-coding exons have been identified, indicating the existence of alternative promoters. One of these is G/C rich and possesses a consensus initiator sequence as well as potential Sp1 binding sites. Expression of exon 1 from this promoter occurs in a wide variety of tissues, whereas expression of the alternative 5' untranslated region (exon 1a) is normally restricted to liver, the principal source of sLIF-R. During pregnancy expression of exon 1a becomes detectable also in the uterus. Expression of exon 1a increases dramatically during gestation and is accompanied by a similar quant. rise in expression of sLIF-R mRNA. These ***findings*** establish that expression of LIF-R is under complex transcriptional control and indicate that regulated expression of the sol. cytokine receptor isoform may be due principally to an increase in the activity of a dedicated promoter.
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 48 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1998:30656 CAPLUS
DN 128:151708
TI Alternative mRNA splicing of 3'-terminal exons generates ascorbate peroxidase isoenzymes in spinach (Spinacia oleracea) chloroplasts
AU Ishikawa, Takahiro; Yoshimura, Kazuya; Tamoi, Masahiro; Takeda, Toru; Shigeoka, Shigeru
CS Department of Food and Nutrition, Faculty of Agriculture, Kinki University, Nara, 631, Japan
SO Biochemical Journal (1997), 328(3), 795-800 CODEN: BIJOAK; ISSN: 0264-6021
PB Portland Press Ltd.
DT Journal
LA English
AB We have isolated two cDNA clones encoding spinach (Spinacia oleracea) stromal and thylakoid-bound ascorbate peroxidase isoenzymes (Ishikawa, T., et al., 1996). The gene (ApxII) encoding both chloroplastic ascorbate peroxidase isoenzymes was isolated and the organization of the gene was detd. Alignment between the cDNAs and the gene for chloroplastic ascorbate peroxidase isoenzymes indicates that both enzymes arise from a common pre-mRNA by alternative splicing of two 3'-terminal exons. Genomic Southern-blot anal. supported this ***finding*** . The gene spanned nearly 8.5 kbp and contained 13 exons split by 12 introns. The penultimate exon 12 (residues 7376-7530) for the stromal ascorbate peroxidase mRNA consisted of one codon for Asp365 before the TAA termination codon, and the entire 3'-untranslated region, including a potential ***polyadenylation*** ***signal*** (AATAAA). The final exon 13 (residues 7545-7756) for the thylakoid-bound ascorbate peroxidase mRNA consisted of the corresponding coding sequence of the hydrophobic C-terminal region, the TGA termination codon and the entire 3'-untranslated region, including a potential ***polyadenylation*** ***signal*** (AATATA). Both exons were interrupted by a 14 bp non-coding sequence. Northern-blot and reverse transcription-PCR anal. showed that the transcripts for stromal and thylakoid-bound ascorbate peroxidase are present in spinach leaves.
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 49 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:775365 CAPLUS
DN 128:99280
TI Isolation of a rat histidase cDNA sequence and expression in Escherichia coli. Evidence of extrahepatic/epidermal distribution
AU Sano, Hirofumi; Tada, Toyohiro; Moriyama, Akihiko; Ogawa, Hisamitsu; Asai, Kiyofumi; Kawai, Yoko; Hodgson, Mark Emory; Kato, Taiji; Wada, Yoshiro; Suchi, Mariko
CS Department of Pediatrics, Nagoya City University Medical School, Nagoya, Japan
SO European Journal of Biochemistry (1997), 250(1), 212-221 CODEN: EJBCAI; ISSN: 0014-2956
PB Springer-Verlag
DT Journal

LA English
AB Histidase (histidine ammonia-lyase) is a cytosolic enzyme responsible for catalyzing the non-oxidative deamination of histidine to urocanic acid. Full-length cDNAs encoding rat histidase have been isolated from a .lambda.ZAP liver cDNA library using a partial cDNA fragment obtained by PCR. Whereas the initial description of the rat histidase 3' untranslated sequence contained a rare ***polyadenylation*** ***signal*** sequence, the data presented encompass a more distant 28-bp region, possessing a nucleotide stretch (AATATAAA), identical to that in the mouse histidase cDNA. Dideoxynucleotide chain-termination sequencing of two clones obtained by in vivo excision yielded an addnl. 376 bp and 105 bp of 5' and 3' untranslated sequences, resp. A selected rat histidase cDNA clone was introduced into the pET-16b prokaryotic vector and expressed in BL21 (DE3)pLysS Escherichia coli. After purifn. by nickel-chelation chromatog., recombinant histidine-tagged protein was employed to raise anti-(rat histidase) Ig in a Japanese white rabbit. The polyclonal rabbit antibody recognized and formed immune complexes with rat and recombinant human histidase proteins. Immunoblots of crude rat organ exts. detected a spectrum of histidase expression extending beyond that obsd. in liver and skin. Among other histidase-pos. cells were those of the renal cortex tubular epithelium, fundic mucosal glands of stomach, gastric i.m. (Auerbach's) plexus, and adrenal cortex. Immunohistochem. studies of histidase in rat liver produced discrete staining of hepatocytes in assocn. with portal triads (Rappaport zone I). Furthermore, in contrast with previous reports of activity confined to epidermal stratum corneum, the ***findings*** demonstrate immunoreactive protein within and limited to the adjacent stratum granulosum.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 50 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:689247 CAPLUS
DN 128:10836
TI cis-Acting signals involved in termination of vesicular stomatitis virus mRNA synthesis include the conserved AUAC and the U7 ***signal*** for ***polyadenylation***
AU Barr, John N.; Whelan, Sean P. J.; Wertz, Gail W.
CS Department of Microbiology, University of Alabama at Birmingham, Birmingham, AL, 35294, USA
SO Journal of Virology (1997), 71(11), 8718-8725 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB We investigated the cis-acting sequences involved in termination of vesicular stomatitis virus mRNA synthesis by using bicistronic genomic analogs. All of the cis-acting signals necessary for termination reside within the first 13 nucleotides of the 23-nucleotide conserved gene junction. This 13-nucleotide termination sequence at the end of the upstream gene comprises the tetranucleotide AUAC, the tract contg. seven uridines (U7 tract), and the intergenic dinucleotide (GA), but it does not include the downstream gene start sequence. Data presented here show that upstream mRNA termination is independent of downstream mRNA initiation. Alteration of any nucleotide in the 13-nucleotide sequence decreased the termination activity of the gene junction and resulted in increased synthesis of a bicistronic readthrough RNA. This ***finding*** indicated that the wild-type gene junction has evolved to achieve the max. termination efficiency. The most crit. position of the AUAC sequence was the C, which could not be altered without complete loss of mRNA termination. Reducing the length of the wild-type U7 tract to zero, five, or six U residues also totally abolished mRNA termination, resulting in exclusive synthesis of the bicistronic readthrough mRNA. Shortening the wild-type U7 tract to either five or six U residues abolished VSV polymerase slippage during readthrough RNA synthesis. Since neither the U5 nor U6 template was able to direct mRNA termination, these data imply that polymerase slippage is a prerequisite for termination. Evidence is also presented to show that in addn. to causing polymerase slippage, the U7 tract itself or its poly(A) product constitutes an essential signal for mRNA termination.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 51 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:676173 CAPLUS
DN 128:30862
TI Characterization of the early region 4 of porcine adenovirus type 3
AU Reddy, P. Seshidhar; Idamakanti, Neeraja; Derbyshire, J. Brian; Nagy, Eva
CS Dep. Pathobiol., Univ. Guelph, Guelph, N1G 2W1, Can.
SO Virus Genes (1997), 15(1), 87-90 CODEN: VIGEET; ISSN: 0920-8569
PB Kluwer
DT Journal
LA English
AB The nucleotide sequence of a 3028 bp DNA segment, located between map coordinates 100 and 92 in the genome of porcine adenovirus type 3 (PAV-3), was detd. The segment includes the entire early region 4 (E-4) and the right inverted terminal repeat sequences. There were to TATA boxes and one canonical ***polyadenylation*** ***signal*** on the 1 strand. Homol. ***searches*** of the GenBank data base for the predicted amino acid sequences revealed that, of the eight open reading frames (ORFs) on the 1 strand, and four ORFs on the r strand, only ORF8 on the 1 strand showed homol. with the 34 kDa E-4 protein of human adenovirus types 2, 12 and 34. Northern blot anal. showed that transcription from the E-4 region of PAV-3 began 4 h after infection, peaked at 8 h and declined after 10 h, before DNA replication began 16 h after infection. The E-4 region of PAV-3 was further characterized by 5' and 3' end mapping of the transcription unit.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 52 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:641369 CAPLUS
DN 127:314908
TI Examination of guinea pig luteinizing hormone-releasing hormone gene reveals a unique decapeptide and existence of two transcripts in the brain
AU Jimenez-Linan, Mercedes; Rubin, Beverly S.; King, Joan C.
CS Department Anatomy Cellular Biology, Tufts University Schools Medicine, Boston, MA, 02111, USA
SO Endocrinology (1997), 138(10), 4123-4130 CODEN: ENDOAO; ISSN: 0013-7227
PB Endocrine Society
DT Journal
LA English
AB We sequenced the complementary DNA (cDNA) encoding guinea pig LHRH from an expression library derived from the preoptic area-anterior hypothalamus. Data from in situ hybridization and RNase protection assays verified that the cloned cDNA was complementary to guinea pig LHRH mRNA. The architecture of the deduced precursor resembles that of LHRH precursors identified in other species. In contrast, the predicted sequence of the decapeptide differs from mammalian LHRH by two amino acid substitutions in positions 2 and 7. This is a novel

finding , because the amino acid sequence that comprises LHRH decapeptide is identical in all mammals studied to date. Moreover, the predicted substitution in amino acid position 2 is unique among vertebrates. A second observation of potential significance is the existence of two subspecies of LHRH mRNA differing only in the length of their 3' untranslated regions. These two transcripts were verified by sequence anal. of pos. clones from the cDNA library and by RNase protection anal. of preoptic area-anterior hypothalamus exts., and their presence is consistent with the two ***polyadenylation*** ***signals*** identified in the untranslated regions of the LHRH gene. Future studies will examine LHRH genes expression in guinea pigs, which like primates but unlike rats, have a true luteal phase as a component of their reproductive cycle.

L5 ANSWER 53 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:347889 CAPLUS
DN 127:61542
TI Regulation of tRNA suppressor activity by an intron-encoded ***polyadenylation*** ***signal***
AU Liang, Songlin; Briggs, Michael W.; Butler, J. Scott
CS Department Microbiology Immunology, University Rochester School Medicine Dentistry, Rochester, NY, 14618, USA
SO RNA (1997), 3(6), 648-659 CODEN: RNARFU; ISSN: 1355-8382
PB Cambridge University Press
DT Journal
LA English
AB A 26-nt sequence from the 3' UTR of the yeast GAL7 mRNA directs accurate and efficient cleavage and polyadenylation to form the 3' end of the GAL7 mRNA in vivo and in vitro. Here we asked whether this ***polyadenylation*** ***signal*** can function within the context of a tRNA. Insertion of the GAL7 signal into the intron of the dominant SUP4 nonsense suppressor allowed us to judge the effect of the insert on SUP4 function by observation of nonsense suppression efficiency in vivo. The GAL7 signal impairs the function of SUP4 in an orientation-dependent manner in vivo, consistent with its ability to specify cleavage and polyadenylation in this context in vitro. Mutation of a UA repeat within the GAL7 signal restores SUP4 function partially, consistent with the role of this repeat as an efficiency element in polyadenylation. Mutations that impair the mRNA 3' end-processing factors Rna14p and Rna15p restore suppressor function partially. Northern blot anal., PCR amplification, and DNA sequence anal. show that the GAL7 ***signal*** directs ***polyadenylation*** within the body of pre-SUP4 and within the terminator, suggesting that polyadenylation inhibits 5' and 3' end processing, as well as removal of the pre-tRNA intron. These ***findings*** indicate that the GAL7 ***polyadenylation*** ***signal*** is capable of targeting a pre-tRNA to the mRNA processing pathway.

L5 ANSWER 54 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:208269 CAPLUS
DN 126:221696
TI Insecticidal toxins of Bacillus thuringiensis in plant protection
AU Misztal, Lucyna Honorata; Musial, Wojciech Grzegorz; Augustyniak, Jacek
CS Pol.
SO Postepy Mikrobiologii (1996), 35(3), 275-293 CODEN: PMKMAV; ISSN: 0079-4252
PB Polskie Towarzystwo Mikrobiologow
DT Journal; General Review
LA Polish
AB A review and discussion with 166 refs. B. thuringiensis is a soil bacterium that during sporulation produces crystals composed of .delta.-endotoxins. An important feature of .delta.-endotoxins is their specificity. Individual toxins usually kill only the larval stage of certain species of insects. Com. prepns. of B. thuringiensis have been widely used as pesticides for >2 decades. The conventional prepns. of B. thuringiensis, however, are quickly degraded by sun light, wind, changes of temp., and humidity. Some problems are also assocd. with the control of insects feeding in vascular systems of inside fruits. These problems may be overcome by the use of transgenic plants. The .delta.-endotoxin genes have been successfully engineered into several plants (for example, maize, tobacco, potato). These studies indicated, however, that the .delta.-endotoxin genes were expressed at extremely low levels. The toxin genes contain many regions characteristic for bacteria (long AT stretches some of which in eukaryotic cells can function as potential ***polyadenylation*** ***signals***) that cause low expression of unmodified genes in plant cells. Introduction of a large no. of translationally neutral mutations in the coding region results in a significant increase in the .delta.-endotoxin level in transgenic plants. One problem assocd. with the use of transgenic plants is the possibility of developing resistance against .delta.-endotoxins in the insect pests. The likelihood of insect resistance, however, is considered to be remote because the mode of action of .delta.-endotoxins is very complex. Several strategies for delaying resistance were proposed: ***searching*** for new .delta.-endotoxin genes and using .delta.-endotoxins in combination with other insect control measures.

L5 ANSWER 55 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:197204 CAPLUS
DN 126:274622
TI Promoter-proximal poly(A) sites are processed efficiently, but the RNA products are unstable in the nucleus
AU Scott, Jeannine M.; Imperiale, Michael J.
CS Department of Microbiology and Immunology, University of Michigan Medical School, Ann Arbor, MI, 48109-0620, USA
SO Molecular and Cellular Biology (1997), 17(4), 2127-2135 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB The presence of two ***polyadenylation*** ***signals*** in the primary transcript of the human immunodeficiency virus type 1 (HIV-1) provirus leads to a requirement for regulation of 3'-end processing. To ensure that viral genome replication and gene expression occur, polyadenylation must occur at the poly(A) site transcribed from the 3' long terminal repeat (LTR) but not the 5' LTR. Models that have been proposed to explain this regulation include (i) inhibition of the 5' site as a result of proximity to the promoter and (ii) enhancement of the 3' site by U3 sequences that are transcribed upstream of only the 3' poly(A) site. In previous studies designed to investigate these models, a redn. in the levels of steady-state RNA was obsd. when the HIV-1 poly(A) site was placed within 500 nucleotides of the cap site. Although these ***findings*** were interpreted to be the result of promoter proximity effects on 3'-end processing, in vitro studies demonstrated that the HIV-1 poly(A) site was equally functional in promoter-proximal and promoter-distal positions. These results led to the hypothesis that, in vivo, the poly(A) site is fully active at this close distance but the short transcripts produced are highly unstable in the nucleus and undergo rapid degrdn., precluding their appearance as abundant mRNAs in the steady-state pool. To investigate the biogenesis of these short RNAs in vivo, expts. were performed to examine directly the nuclear processing rates of the HIV-1 poly(A) site in intact cells. By using recombinant adenoviruses as expression vectors, it is now demonstrated conclusively that the HIV-1 poly(A) site is indeed

processed at equiv. levels independent of its distance from the promoter. Although transcripts contg. the promoter-proximal poly(A) site are processed efficiently, most undergo degrdn. in the nucleus instead of nucleocytoplasmic transport.

L5 ANSWER 56 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:145247 CAPLUS
DN 126:139878
TI Cell adhesion molecule C-CAM expression vectors and cancer therapy and diagnosis
IN Hsieh, Jer-Tsong; Lin, Sue-Hwa
PA Board of Regents, University of Texas System, USA; Hsieh, Jer-Tsong; Lin, Sue-Hwa
SO PCT Int. Appl., 141 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---- ---------- ---- -------- ---------- --------
PI WO 9700954 A1 19970109 WO 1996-US10696 19960621 W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA AU 9663905 A1 19970122 AU 1996-63905 19960621
PRAI US 1995-494622 19950623 WO 1996-US10696 19960621
AB A variety of genetic constructs are disclosed that will ***find*** both in vitro and in vivo use in the area of tumor biol. and cancer therapy. In particular, expression constructs are provided that contain a C-CAM encoding region and other regulatory elements necessary for the expression of a C-CAM transcript. One version of the expression construct is a replication-deficient adenoviral vector. Also provided are methods for the transformation of cell lines and the inhibition of cancer cell proliferation.

L5 ANSWER 57 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:113169 CAPLUS
DN 126:100144
TI Probing the 3' UTR Structure of U1A mRNA and Footprinting Analysis of Its Complex with U1A Protein
AU Teunissen, Sander W. M.; van Gelder, Celia W. G.; van Venrooij, Walther J.
CS Department of Biochemistry, University of Nijmegen, Nijmegen, 6500 HB, Neth.
SO Biochemistry (1997), 36(7), 1782-1789 CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
AB The structure of the conserved region of the U1A pre-mRNA (Ag RNA) and its complex with U1A protein was investigated. The previously proposed secondary structure of Ag RNA, derived from enzymic probing and anal. of the structure and function of mutant mRNAs, is now confirmed by chem. probing data and further refined in the regions where the enzymic data were not conclusive. The two unpaired nucleotides in the internal loops opposite of the Box sequences as well as the tetraloop could not be cleaved by RNases, but are accessible to chem. probes. Concerning the RNA-protein complex, the protection expts. showed that the Box regions are largely protected when the U1A protein is present. All stem regions in the 5' part of the structure seem protected against RNases. Unexpectedly, the nucleotides of the tetraloop become accessible to RNases in the RNA-protein complex. This result indicates that the tetraloop undergoes a conformational change upon U1A protein binding. The 3' part of the Ag RNA sequence, contg. the ***polyadenylation*** ***signal*** in a hairpin structure, showed hardly any protection, a ***finding*** that agrees with the fact that U1A does not interfere with the binding of the cleavage polyadenylation specificity factor (CPSF) to the ***polyadenylation*** ***signal*** .

L5 ANSWER 58 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1997:25627 CAPLUS
DN 126:71136
TI Cloning, cDNA sequence, and alternative splicing of porcine amelogenin mRNAs
AU Hu, C -C.; Bartlett, J. D.; Zhang, C. H.; Qian, Q.; Ryu, O. H.; Simmer, J. P.
CS School Dentistry, University Texas, San Antonio, TX, 78284-7888, USA
SO Journal of Dental Research (1996), 75(10), 1735-1741 CODEN: JDREAF; ISSN: 0022-0345
PB International Association for Dental Research
DT Journal
LA English
AB In mammals, the org. matrix of developing enamel is dominated by amelogenins. To investigate the expression of proteins secreted into the developing enamel matrix, we have constructed a porcine enamel organ epithelia-specific cDNA library. The amelogenin fraction of the cDNA library was characterized by the cloning of amelogenin-specific polymerase chain-reaction (PCR) amplification products, 5' and 3' rapid amplification of cDNA ends (RACE), and by helper phage rescue of unamplified clones. Clones were characterized that encode porcine amelogenin isoforms 173, 157, 56, 41, and 40 amino acids in length. The structure of the porcine amelogenin gene differs from that of any of those yet described. There are two homologous but distinct exons 1, 2, and 7. One of the two exon 7s can vary in length depending upon the selection of either of two ***polyadenylation*** ***signal*** /cleavage sites. As a rule, a given exon 1 always pairs with the same exon 2 but can be assocd. with either exon 7. Despite significant sequence divergence within these exons, no differences are obsd. in exons 3, 5, and 6. We interpret these ***findings*** as evidence of a single amelogenin gene expressed from two promoters; however, the results do not exclude the existence of a second amelogenin gene. The variability generated through the use of alternate promoters and exon 7s primarily affects the non-coding regions of the message. A given amelogenin isoform expressed from the two promoters displays four amino acid differences within the signal peptide, while the secreted proteins are identical. Similarly, the alternative use of exon 7 does not alter the structure of the protein products. The pattern of RNA splicing of amelogenin pre-mRNAs is different for the transcripts expressed from the two promoters. The 173- and the 56-residue amelogenins can be expressed from either promoter, while the 157-residue amelogenin is generated by only one of the two promoters.
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 59 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:746908 CAPLUS
DN 126:71705
TI Mouse cytoplasmic polyadenylylation element binding protein: an evolutionarily conserved protein that interacts with the cytoplasmic polyadenylylation elements of c-mos mRNA
AU Gebauer, Fatima; Richter, Joel D.
CS Worcester Foundation Biomed. Res., Shrewsbury, MA, 01545, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1996), 93(25), 14602-14607 CODEN: PNASA6; ISSN: 0027-8424

PB National Academy of Sciences
DT Journal
LA English
AB Cytoplasmic polyadenylylation is an essential process that controls the translation of maternal mRNAs during early development and depends on two cis elements in the 3' untranslated region: the polyadenylylation hexanucleotide AAUAAA and a U-rich cytoplasmic polyadenylylation element (CPE). In ***searching*** for factors that could mediate cytoplasmic polyadenylylation of mouse c-mos mRNA, which encodes a serine/threonine kinase necessary for oocyte maturation, the authors have isolated the mouse homolog of CPEB, a protein that binds to the CPEs of a no. of mRNAs in Xenopus oocytes and is required for their polyadenylylation. Mouse CPEB (mCPEB) is a 62-kDa protein that binds to the CPEs of c-mos mRNA. MCPEB mRNA is present in the ovary, testis, and kidney; within the ovary, this RNA is restricted to oocytes. MCPEB shows 80% overall identity with its Xenopus counterpart, with a higher homol. in the carboxyl-terminal portion, which contains two RNA recognition motifs and a cysteine/histidine repeat. Proteins from arthropods and nematodes are also similar to this region, suggesting an ancient and widely used mechanism to control polyadenylylation and translation.

L5 ANSWER 60 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:576417 CAPLUS
DN 125:239767
TI Genomic organization of the mouse .beta.1 gene: conservation of the .beta.1D but not of the .beta.1B and .beta.1C integrin splice variants
AU Baudoin, Christian; Van Der Flier, Arjan; Borradori, Luca; Sonnenberg, Arnoud
CS Department of Cell Biology, Netherlands Cancer Institute, Amsterdam, 1066 CX, Neth.
SO Cell Adhesion and Communication (1996), 4(1), 1-11 CODEN: CADCEF; ISSN: 1061-5385
PB Harwood
DT Journal
LA English
AB The authors have detd. the genomic organization of the 3'-region of the murine .beta.1 gene and cloned the murine .beta.1D integrin splice variant. Overlapping genomic clones encompassing the region of the .beta.1D-specific exons were isolated from a phage .lambda. FIXII library, mapped and partially sequenced. All of the exon-intron junctions identified in the murine .beta.1 gene fit with the consensus splice donor and acceptor sequences and occur at the same positions as in their human counterparts. CDNA clones for the .beta.1D integrin were isolated from a murine skeletal muscle library. The human and murine .beta.1D sequences are conserved at the nucleotide (93%) and amino acid (100%) level, suggesting an important role of this muscle-specific variant throughout mammalian phylogenesis. In contrast, murine sequences for .beta.1B are very different from human .beta.1B at both the nucleotide as well as amino acid level. Moreover, no specific ***polyadenylation*** ***signal*** for the .beta.1B variant could be identified in genomic clones, suggesting that this variant is not present in the mouse. Finally, the authors were not able to identify a murine .beta.1C splice variant by sequencing anal., Southern hybridization techniques or polymerase chain reaction of mRNA from platelets. These ***findings*** indicate that the .beta.1B and .beta.1C variants emerged relatively late in the phylogenesis of the .beta.1 integrin family.

L5 ANSWER 61 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:568158 CAPLUS
DN 125:217622
TI TIMP-3 is expressed in the human retinal pigment epithelium
AU Ruiz, Alberto; Brett, Peterson; Bok, Dean
CS Dep. Neurobiol., Jules Stein Eye Inst., Univ. California, Los Angeles, CA, 90024, USA
SO Biochemical and Biophysical Research Communications (1996), 226(2), 467-474 CODEN: BBRCA9; ISSN: 0006-291X
PB Academic
DT Journal
LA English
AB TIMP-3 is the most recent member of the tissue inhibitor of metalloproteinases (TIMP) family. In the present study, we describe the expression of TIMP-3 mRNA (mRNA) by the retinal pigment epithelium of the normal human eye (hRPE). In addn. to the three predominant transcripts of approx. 5.1, 2.8, and 2.4 Kbp found in several other human tissues at adult and fetal stages. The hRPE also expresses two RNA species of 1.2 and 1.0 Kbp. Based on the sequence anal. of cDNA clones isolated from a hRPE cDNA library, the use of alternate ***polyadenylation*** ***signals*** could account for the expression of these smaller transcripts. The possibility of an alternative mechanism of regulation of the expression of TIMP-3 by the RPE is not discarded. The no. of RNA transcripts specific for TIMP-3 per ng of poly A+RNA was quantified by RT-PCR. 9.6 .times. 105 transcripts per ng of polyA+RNA were found at the adult stage and 1.2 .times. 106 transcripts per ng of polyA+RNA were detected at the fetal stage. These ***findings*** were supported by the predominant labeling in the RPE layer of retinal tissue sections in in situ hybridization expts. All of these data support the hypothesis that the prodn. of TIMP-3 by the RPE may be crucial for the maintenance of Bruch's membrane, the complex layer of extracellular matrix that provides a structural substrate for the RPE in the healthy retina and is perturbed during the ageing process and in Sorsby's Fundus Dystrophy, a dominantly inherited disease.

L5 ANSWER 62 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:381056 CAPLUS
DN 125:76753
TI Testosterone regulates tissue-specific changes in the binding of a 47-kilodalton protein to a highly conserved sequence in the 3' untranslated region of epidermal growth factor messenger ribonucleic acid
AU Sheflin, Lowell G.; Brooks, Elizabeth M.; Spaulding, Stephen W.
CS Res. Service VA Western New York Healthcare System, Dep. Med., State Univ. New York, Buffalo, Buffalo, NY, 14215, USA
SO Endocrinology (1996), 137(7), 2910-2917 CODEN: ENDOAO; ISSN: 0013-7227
PB Endocrine Society
DT Journal
LA English
AB Epidermal growth factor (EGF) transcripts that use the terminal ***polyadenylation*** ***signal*** display a dramatic sex difference in the pattern of polyadenylation in the murine submaxillary gland (SMG), whereas those in the kidney do not. It takes 3 days before testosterone treatment begins to change the polyadenylation pattern in female SMG to resemble the male pattern, a ***finding*** that supports previous suggestions that posttranscriptional mechanisms are involved in regulating EGF expression. The conservation of a unique 23-b sequence centered on the terminal ***polyadenylation*** ***signal*** in all published mammalian EGF sequences suggested that trans-acting factors involved in EGF mRNA metab. might bind to this sequence. To investigate this, we prepd. 32P-RNA contg. the 3' terminal EGF 23-b sequence plus a short poly-A tail, and incubated it with SMG cytosol. Cytosol retarded the electrophoretic mobility of this RNA as a single prominent band

on 8% PAGE, and by UV-crosslinking, a single prominent 47-kDa protein was detected on 10% SDS-PAGE. Trypsin abolished both the gel-retarding and crosslinking activities. Cytosol from female SMGs contained approx. 8 times more of both the RNA binding activities than male cytosol. Injecting testosterone (200 .mu.g QOD) into female mice altered both the RNA binding activities in a biphasic fashion, initially increasing them by about 40% at 2 days, then decreasing them by about 65% .gtoreq. 5 days, reaching male levels. Kidney cytosol contained both RNA binding activities but displayed neither sexual dimorphism nor testosterone-responsiveness. The tissue-specific testosterone-dependent changes obsd. in the 47-kDa protein occur before the increase in EGF mRNA levels and before the change in EGF mRNA polyadenylation, so this cytosolic protein could be a trans-acting factor involved in EGF polyadenylation.

L5 ANSWER 63 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:327659 CAPLUS
DN 125:27325
TI Cloning a cDNA for carbonyl reductase (Cbr) from mouse cerebellum: murine genes that express Cbr map to chromosomes 16 and 11
AU Wei, Jianjun; Dlouhy, Stephen R.; Hara, Akira; Ghetti, Bernardino; Hodes, M. E.
CS Dep. Pathol. Lab. Med., Indiana Univ. Sch. Med., Indianapolis, IN, 46202, USA
SO Genomics (1996), 34(1), 147-148 CODEN: GNMCEP; ISSN: 0888-7543
PB Academic
DT Journal
LA English
AB The human CBR1 cDNA was used to isolate and purify several putative murine Cbr1 genomic clones. A 3.1-kb EcoRI DNA fragment hybridized with the probe. This band was cloned, and both ends were partially sequenced. A ***search*** for homologous sequences showed that a mouse DNA sequence of 197 bp was highly homologous to the 3' end of the human CBR1 cDNA. The 197-bp segment was subcloned and used to probe a Northern blot. A 1.2-kb mRNA band was detected in adult mouse liver, cerebrum, cerebellum, and testis. The latter had an addnl. large band (1.5 kb) that might have come from an alternatively spliced transcript. Mouse liver and cerebellum showed approx. twice the amt. of CBR RNA as brain or testis. We synthesized and antisense oligonucleotide, 5'-TCCTTGGCCTTCAOCAAGTC-3' from the 3' end of the mouse Cbr1 gene that was used for rapid amplification of cDNA ends (RACE) from adult mouse cerebellar mRNA, with a specific 3' antisense primer and adapter primer (Clontech). Two distinct cDNA bands, about 1000 and 550 bp, were generated. These were cloned, and both strands were sequenced. The full-length cDNA contains 1052 bp and an open reading frame of 831 bp, corresponding to 277 amino acids, and extends from the ATC start codon at position 128 to the TGA stop codon at position 961. The smaller RACE product represents the 3' end of the full-length cDNA. The 5' and 3 noncoding regions of the full-length cDNA contain 127 and 91 bp, including a GC-rich 5'-flanking region and a 3' ***polyadenylation*** ***signal*** , AATAAA. The cDNA shows 82, 91, and 81% homol. to human, rat, and rabbit Cbr1 genes, whereas the deduced amino acid sequence shows 91, 93, and 88% homol., resp.

L5 ANSWER 64 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:317218 CAPLUS
DN 125:2871
TI Sequence of the polypyrimidine tract of the 3'-terminal 3' splicing signal can affect intron-dependent pre-mRNA processing in vivo
AU Liu, Xuedong; Mertz, Janet E.
CS McArdle Laboratory Cancer Research Laboratory Genetics, University Wisconsin, Madison, WI, 53706-1599, USA
SO Nucleic Acids Research (1996), 24(9), 1765-1773 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB Most pre-mRNAs require an intron for efficient processing in higher eukaryotes. However, not all introns can provide this function. For example, transcripts synthesized from a variant of the human .beta.-globin gene lacking its second intervening sequence (IVS2), yet retaining its first intervening sequence (IVS1), exhibit multiple defects in mRNA biogenesis. To investigate why, we transfected into monkey cells plasmids contg. the human .beta.-globin gene and variants of it altered in (i) IVS1, (ii) the 3'-terminal exon, and (iii) the ***polyadenylation*** ***signal*** . The .beta.-globin RNAs accumulated in these cells were analyzed by quant. S1 nuclease mapping for nuclear accumulation, intron excision, polyadenylation and cytoplasmic accumulation. We found that the 3' splicing signal of IVS1, with multiple purines interrupting its polypyrimidine tract, could efficiently function as an internal 3' splicing signal; however, it could not efficiently function as the 3'-terminal 3' splicing signal for any of these steps in intron-dependent mRNA biogenesis unless (i) its polypyrimidine tract was made uninterrupted in pyrimidines, or (ii) specific sequences were deleted from the 3'-terminal exon. We conclude that whether an intron can provide the function necessary for efficient processing of intron-dependent pre-mRNA is dependent upon the ability of its 3' splicing signal to define the 3'-terminal exon. On the practical side, this ***finding*** means one needs to consider both the sequence and location of the intron to be included in an intron-dependent gene to obtain efficient expression in vivo.

L5 ANSWER 65 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:314915 CAPLUS
DN 125:2847
TI Signals sufficient for 3'-end formation of yeast mRNA
AU Guo, Zijian; Sherman, Fred
CS Dep. Biochem., Univ. Rochester Sch. Med. Dent., Rochester, NY, 14642, USA
SO Molecular and Cellular Biology (1996), 16(6), 2772-2776 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB The following three elements were previously shown to be required for 3'-end formation of mRNA in the yeast Saccharomyces cerevisiae: (i) the efficiency element TATATA or related sequences, which function by enhancing the efficiency of downstream positioning elements; (ii) the positioning element AATAAA or related sequences, which position the poly(A) site; and (iii) the actual poly(A) site, which is usually Py(A)n. In this study, we synthesized a 39-bp poly(A) signal that contained the optimum sequences of these three elements. By inserting the synthetic 3'-end-forming signal into various positions of a CYC1-lacZ fusion gene, we showed that truncated transcripts of the expected sizes were generated. Furthermore, the poly(A) sites of the truncated transcripts were mapped to the expected poly(A) site within the synthetic signal. Our ***findings*** establish that the three elements are not only necessary but also sufficient for mRNA 3'-end formation in S. cerevisiae.

L5 ANSWER 66 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:314894 CAPLUS
DN 125:2837

TI The cap and the 3' splice site similarly affect polyadenylation efficiency
AU Cooke, Charles; Alwine, James C.
CS Sch. Med., Univ. Pennsylvania, Philadelphia, PA, 19104-6142, USA
SO Molecular and Cellular Biology (1996), 16(6), 2579-2584 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB The 5' cap of a mammalian pre-mRNA has been shown to interact with splicing components at the adjacent 5' splice site for processing of the first exon and the removal of the first intron. Likewise, it has been shown that processing of the last exon and removal of the last intron involve interaction between splicing components at the 3' splice site and the polyadenylation complex at the ***polyadenylation*** ***signal*** . These ***findings*** suggest that the cap provides a function in first exon processing which is similar to the function of the 3' splice site in last exon processing. To det. whether caps and 3' splice sites function similarly, we compared the effects of the cap and the 3' splice site on the in vitro utilization of the simian virus 40 late ***polyadenylation*** ***signal*** . We show that the presence of a m7GPPPG cap, but not a cap analog, can pos. affect the efficiency of polyadenylation-only substrate. Cap analogs do not stimulate polyadenylation because they fail to bind titratable cap-binding factors. The failure of cap analogs to stimulate polyadenylation can be overcome if a 3' splice site is present upstream of the ***polyadenylation*** ***signal*** . These data indicate that factors interacting with the cap or the 3' splice site function similarly to affect polyadenylation efficiency and complete exon processing. We also ***find*** that a 5' splice site directly upstream of the ***polyadenylation*** ***signal*** , along with a m7GppG cap, is inhibitory to polyadenylation. This ***finding*** suggests that the interaction between the cap-binding complexes and splicing components at the 5' splice site may form a complex which is inhibitory to further processing if splicing of an adjacent intron is not achieved.

L5 ANSWER 67 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:171414 CAPLUS
DN 124:256575
TI Genetic organization, size, and complete sequence of early region 3 genes of human adenovirus type 41
AU Yeh, Hung-Yueh; Pieniazek, Norman; Pieniazek, Danuta; Luftig, Ronald B.
CS Department Microbiology, Louisiana State University Medical Center, New Orleans, LA, 70112, USA
SO Journal of Virology (1996), 70(4), 2658-63 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB The complete nucleotide and predicted amino acid sequences for open reading frames (ORFs) of the human adenovirus type 41 (Ad41) early region 3 (E3) gene have been detd. The sequence of the Ad41 E3 gene (map units 74 to 83.9) consists of 3,373 nucleotides and has one TATA box and two ***polyadenylation*** ***signals*** (AATAAA). Anal. of the nucleotide sequence reveals that the E3 gene can encode six ORFs, designated RL1 to RL6. These are all expressed at the mRNA level, as detd. by reverse transcription-PCR anal. of Ad41-infected cell RNA. When compared with known E3 sequences of most other human adenoviruses deposited in GenBank, the sequences of RL1 to RL3 were found to be unique to subgroup F adenoviruses (Ad40 and Ad41). They encode putative proteins of 173 amino acids (19.4 kDa) and 276 amino acids (31.6 kDa) in one reading frame as well as a 59-amino-acid (6.7 kDa) protein in an overlapping reading frame. RL4 encodes a 90-amino-acid protein (10.1 kDa) with 40% homol. to the Ad2 E3 10.4-kDa protein, which induces degrdn. of the epidermal growth factor receptor and functions together with the Ad2 E3 14.5-kDa protein to protect mouse cell lines against lysis. RL5 encodes a protein of 107 amino acid residues (12.3 kDa) and is analogous to the Ad2 E3 14.5-kDa protein. RL6 codes for a protein of 122 amino acids (14.7 kDa) that is analogous to the Ad2 14.7-kDa protein, which functions to protect Ad-infected cells from tumor necrosis factor-induced cytolysis. This ***finding*** of three unique (RL1 to RL3) E3 gene ORFs may explain why subgroup F adenoviruses differ substantially from other human adenoviruses in their host range; i.e., they replicate predominantly in the host's gastrointestinal rather than respiratory tract. A recent phylogenetic study that compared subgroup F Ad40 DNA sequences with representatives of subgroups B (Ad3), C (Ad2), and E (Ad4) reached a similar conclusion about the uniqueness of RL1 and RL2.

L5 ANSWER 68 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:166592 CAPLUS
DN 124:221378
TI Functional promoter and polyadenylation site mapping of the human serotonin (5-HT) transporter gene
AU Heils, A.; Teufel, A.; Petri, S.; Seemann, M.; Bengel, D.; Balling, U.; Riederer, P.; Lesch, K.-P.
CS Department Psychiatry, University Wurzburg, Germany
SO Journal of Neural Transmission: General Section (1995), 102(3), 247-54 CODEN: JNGSE8; ISSN: 0300-9564
PB Springer
DT Journal
LA English
AB We have isolated and characterized the 5'-flanking region and the proximal polyadenylation site of the human 5-HT transporter gene. The major gene transcript is 2,793bp in length and it contains 208bp of 5'-untranslated region (5'-UTR) and 694 bases of 3'-UTR. While only a single mRNA species occurs in rats and mice, the most proximal ***signal*** for ***polyadenylation*** in the human gene appears to be highly degenerate in comparison to the rat and murine motif. This ***polyadenylation*** ***signal*** -like motif may lead to alternate usage of addnl. polyadenylation sites resulting in multiple mRNA species in humans. A TATA-like motif and several potential binding sites for transcription factors including AP1, AP2, SP1, and a cAMP response element (CRE)-like motif are present in the 5'-flanking region. A .apprxeq.1.7kb fragment beginning 217bp downstream from the transcription start site, which had been ligated into a luciferase reporter vector and transiently expressed in JAR human placental choriocarcinoma cells, displayed both constitutive and forskolin/cholera toxin-induced promoter activity. Functional promoter mapping revealed that there are neg. attenuating elements between bp -1,428 and -1,185 and pos. elements between bp -1,184 and -78 from the transcription initiation site. Studies with deletional mutants also indicated that core promoter sequences are contained within 78bp of the transcription start site and that regulation of cAMP-inducible promoter activity depends on multiple cis-acting elements including two AP1 binding sites and a single CRE-like element located at bp -99. Our ***findings*** suggest that (1) the 5-HT transporter gene promoter is active in human JAR cells, but inactive in 5-HT transporter-deficient human SK-N-SH neuroblastoma and HeLa cells, (2) the information contained within 1.4kb of 5'-flanking sequence is sufficient to confer its cell-specific expression, (3) the promoter responds to cAMP induction, and (4) the expression of the 5-HT transporter gene is regulated

by a combination of pos. and neg. cis-acting elements operating through a basal promoter unit defined by a TATA-like motif.

L5 ANSWER 69 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:110187 CAPLUS
DN 124:168694
TI Interaction between the U1 snRNP-A protein and the 160-kD subunit of cleavage-polyadenylation specificity factor increases polyadenylation efficiency in vitro
AU Lutz, Carol S.; Murthy, Kanneganti G. K.; Schek, Nancy; O'Connor, J. Patrick; Manley, James L.; Alwine, James C.
CS Dep. Microbiology, Univ. Pennsylvania, Philadelphia, PA, 19104, USA
SO Genes & Development (1996), 10(3), 325-37 CODEN: GEDEEP; ISSN: 0890-9369
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB The authors have previously shown that the U1 snRNP-A protein (U1A) interacts with elements in the SV40 late ***polyadenylation*** ***signal*** and that this assocn. increases polyadenylation efficiency. It was postulated that this interaction occurs to facilitate protein-protein assocn. between components of the U1 snRNP and proteins of the polyadenylation complex. The authors have now used GST fusion protein expts., coimmunopptns. and Far Western blot analyses to demonstrate direct binding between U1A and the 160-kDa subunit of cleavage-polyadenylation specificity factor (CPSF). In addn., Western blot analyses of fractions from various stages of CPSF purifn. indicated that U1A copurified with CPSF to a point but could be sepd. in the highly purified fractions. These data suggest that U1A protein is not an integral component of CPSF but may be able to interact and affect its activity. In this regard, the addn. of purified, recombinant U1A to polyadenylation reactions contg. CPSF, poly(A) polymerase, and a precleaved RNA substrate resulted in concn.-dependent increases in both the level of polyadenylation and poly(A) tail length. In agreement with the increase in polyadenylation efficiency caused by U1A, recombinant U1A stabilized the interaction of CPSF with the AAUAAA-contg. substrate RNA in electrophoretic mobility shift expts. These ***findings*** suggest that, in addn. to its function in splicing, U1A plays a more global role in RNA processing through effects on polyadenylation.

L5 ANSWER 70 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:916207 CAPLUS
DN 124:47367
TI Selective use of an alternative stop codon and ***polyadenylation*** ***signal*** within intron sequences leads to a truncated topoisomerase II.alpha. messenger RNA and protein in human HL-60 leukemia cells selected for resistance to mitoxantrone
AU Harker, W. Graydon; Slade, D. Lynn; Parr, Ryan L.; Holguin, Mark H.
CS Medicine Service, Veterans Affairs Medical Center, Salt Lake City, UT, 84148, USA
SO Cancer Research (1995), 55(21), 4962-71 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB Topoisomerase II.alpha. is an essential nuclear enzyme involved in DNA replication and a target for many of the clin. useful antineoplastic agents. In a mitoxantrone-selected human leukemia cell line, HL-60/MX2, cellular topoisomerase II (topo II) catalytic activity is decreased, in assocn. with the ***finding*** of reduced nuclear topo II.alpha. and .beta. protein levels. In addn., HL-60/MX2 cells contain a novel M2 160,000 topo II.alpha.-related protein that localizes predominantly to the cell cytoplasm (W. G. Harker et al., Biochem., 30: 9953-9961, 1991). In these studies, we have investigated the mol. mechanisms underlying the altered expression of the topo II.alpha. protein(s) in these cells. Three topo II.alpha. mRNAs, 7.2, 6.3, and 4.8 kb, were identified in the HL-60/MX2 cells, with the 6.3 and 4.8 kb transcripts being present in roughly equiv. amts., while the 7.2-kb mRNA represents <7% of the total topo II.alpha.-specific mRNA. Portions of the 3'-coding and 3'-untranslated regions were found to be missing from the 7.2- and 4.8-kb topo II.alpha. mRNAs by Northern blot anal. Sequences encoding the 3' regions of the normal and truncated forms of the topo II.alpha. enzyme were obtained from the HL-60/MX2 cells through the use of a 3'-rapid amplification of cDNA ends strategy. Approx. 1321 nucleotides are missing from the 3'-coding and 3'-untranslated regions of the 4.8-kb mRNA and are replaced by 122 nucleotides that contain an inframe stop codon and consensus ***polyadenylation*** ***signal*** . The translation product of the truncated 4388-bp topo II.alpha. transcript would have a predicted Mr of 157,850, with 108 COOH-terminal amino acids being replaced by 13 novel residues. Immunoblot anal. confirmed that amino acids in the COOH-terminal region of topo II.alpha. were missing from the Mr 160,000 HL-60/MX2 protein, and antisera generated to a synthetic peptide representing the 13 unique amino acids identified a Mr 160,000 protein in nuclear exts. from these cells. PCR evaluation of the organization of the 3' region of the topo II.alpha. gene revealed that the 4.8-kb mRNA at a consensus exon-intron splice donor site. The 122-bp novel nucleotides identified in the truncated transcript appear to originate from an adjacent intron as a result of altered RNA processing. These studies suggest that as a result of the disruption of the carboxy terminus of the topo II.alpha. protein and the putative nuclear targeting sequences identified therein, cellular localization of the protein is altered, which may confer a growth advantage for the HL-60/MX2 cells in the presence of mitoxantrone.

L5 ANSWER 71 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:897876 CAPLUS
DN 124:77858
TI DNA sequence and transcriptional analysis of the glycoprotein M gene of murine cytomegalovirus
AU Scalzo, Anthony A.; Forbes, Catherine A.; Davis-Poynter, Nicholas J.; Farrell, Helen E.; Lyons, Paul A.
CS Dep. Microbiology, Univ. Western Australia, Nedlands, 6907, Australia
SO Journal of General Virology (1995), 76(11), 2895-901 CODEN: JGVIAY; ISSN: 0022-1317
PB Society for General Microbiology
DT Journal
LA English
AB The authors have characterized the gene encoding the murine cytomegalovirus (MCMV) homolog of the human cytomegalovirus (HCMV) UL100 open reading frame (ORF) that encodes the HCMV glycoprotein M (gM) mol. It was identified based on its collinearity with MCMV homologues of the HCMV UL99, UL102, UL103, and UL104 ORFs which lie in the HindIII G fragment of the K181 strain of MCMV. Sequencing of a 2.cntdot.3 kb EcoRI-BamHI subfragment of the EcoRI G fragment adjacent to the EcoRI A fragment revealed the presence of the complete MCMV gM ORF and two incomplete ORFs, which corresponded to homologues of HCMV UL99 and UL102. The MCMV gM ORF consists of 1059 nucleotides and is expressed as a 1.cntdot.2 kb transcript at late times post-infection. To precisely characterize the gM transcript, the 5' and 3' ends were mapped. It was found that the transcript initiates at nucleotides 740 or 745, and that

the site of polyadenylation at nucleotide 196 1occurs downstream of the second potential ***polyadenylation*** ***signal*** located at nucleotide 1934. Based on these ***findings*** the MCMV gM is predicted to consist of 353 residues and when compared with HCMV gM has a 47% level of identity. Of great interest is the ***finding*** that the MCMV gM amino acid sequence is completely conserved among six isolates of MCMV that had been shown to exhibit considerable variation both in the MCMV glycoprotein B and the immediate-early 1 gene-encoded pp89 mol. Thus, this glycoprotein appears to be antigenically conserved.

L5 ANSWER 72 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:871810 CAPLUS
DN 124:6083
TI Herpes simplex virus trans-regulatory protein ICP27 stabilizes and binds to 3' ends of labile mRNA
AU Brown, Charles R.; Nakamura, Monica S.; Mosca, Joseph D.; Hayward, Gary S.; Straus, Stephen E.; Perera, L. P.
CS Med. Virol. Section, Natl. Inst. Allergy Infectious Dis., Bethesda, MD, 20892, USA
SO Journal of Virology (1995), 69(11), 7187-95 CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology
DT Journal
LA English
AB Previous work demonstrated that a herpes simplex virus type 1 (HSV-1) immediate-early function upregulates beta interferon but not chloramphenicol acetyltransferase reporter genes driven by the strong simian virus 40 (SV40) or cytomegalovirus promoter-enhancer regions in both transient assays and stable cell lines. The different 3' mRNA stabilization and RNA-processing signals from these two reporter genes appeared to be primarily responsible for this phenomenon. The authors now report that the HSV-1 ICP27 itself is sufficient to stimulate both steady-state accumulation and increased half-life of beta interferon reporter gene mRNA. Furthermore, the ability to respond directly to cotransfected ICP27 can be transferred to chloramphenicol acetyltransferase reporter genes by replacement of their SV40-derived splicing and poly(A) signals with the 3' AU-rich and poly(A) RNA-processing signals from the normally highly labile beta interferon and c-myc mRNA species. ICP27 expressed in bacteria bound specifically to in vitro-generated RNA from both the beta interferon and c-myc intronless AU-rich 3' RNA-processing regions, but not to the SV40-derived early-region splice signal and poly(A) sequences. By site-specific mutagenesis, the authors also show that individual ICP27 C-terminal amino acid residues that are positionally conserved in ICP27 homologs in other herpesviruses (D-357, E-358, H-479, C-400, C-483, and C-488) are crit. for trans-regulatory activity. Importantly, several of these positions match mutations that are known to be essential for the role of ICP27 in the early-to-late switch during the virus lytic cycle. Therefore, our ***findings*** support the notion that HSV ICP27 modulates gene expression posttranscriptionally in part by targeting RNA.

L5 ANSWER 73 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:764946 CAPLUS
DN 123:307755
TI Volvox carteri .alpha.2- and .beta.2-tubulin-encoding genes: regulatory signals and transcription
AU Mages, Wolfgang; Cresnar, Bronja; Harper, Jeffrey F.; Bruederlein, Martina; Schmitt, Ruediger
CS Universitaet Regensburg, Universitaetsstrasse 31, Regensburg, D-93040, Germany
SO Gene (1995), 160(1), 47-54 CODEN: GENED6; ISSN: 0378-1119
PB Elsevier
DT Journal
LA English
AB Microtubules (MT) carry out several specialized morphogenetic functions in the multicellular green alga Volvox carteri (Vc), in addn. to functions also executed in its closest unicellular relative, Chlamydomonas reinhardtii (Cr). To ***find*** out if these differences in morphogenetic complexity are reflected in tubulin (Tub) differences, the Vc .alpha.tub and .beta.tub genes were compared with their Cr counterparts. The Vc genome contains 2 .alpha.tub and 2 .beta.tub genes. This report provides the sequences of the .alpha.2tub and .beta.2tub genes, and thus complete the set of 4 tub sequences. The 2 .alpha.tub and 2 .beta.tub genes code for identical 451 (.alpha.) and 443 (.beta.) amino acid (aa) polypeptides; they differ from the Cr homologs in 2 (.alpha.) and 1 (.beta.) residues, resp. Silent nucleotide (nt) exchanges between sibling genes are much more frequent in Vc than in Cr (12 vs. 2%), probably owing to a more stringent codon bias in the latter alga. Transcription of .alpha.2tub and .beta.2tub starts with an A, 26 bp (.alpha.2) or 25 bp (.beta.2) downstream from the TATA box. A 16-bp promoter element upstream and a G+C-rich sequence downstream from the TATA box are conserved in all tub of both species. Moreover, a 28-bp element of conserved sequence, and hence of possible functional significance, was found at similar locations in the 5' untranslated region (UTR) of all 4 .alpha.tub. A conserved TGTAA downstream from the translation stop codon represents the algal poly(A)-addn. signal (in both Vc and Cr). Northern analyses and reverse transcription (RT) followed by polymerase chain reaction have demonstrated that all 4 tub RNAs are present at all stages of the Vc life cycle.

L5 ANSWER 74 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:755200 CAPLUS
DN 123:195331
TI Polyadenylation polymorphism in the acetyltransferase 1 gene (NAT1) increases risk of colorectal cancer
AU Bell, Douglas A.; Stephens, Elizabeth A.; Castranio, Trisha; Umbach, David M.; Watson, Mary; Deakin, Mark; Elder, James; Hendrickse, C.; Duncan, Hamish; Strange, Richard C.
CS Lab. of Biochemical Risk Analysis and Statistics and Biomathematics Banch, National Inst. of Environmental Health Sciences, Research Triangle Park, NC, 27709, USA
SO Cancer Research (1995), 55(16), 3537-42 CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
AB Exposure to carcinogens present in the diet, cigarette smoke, or the environment may be assocd. with increased risk of colorectal cancer. Arom. amines (aryl- and heterocyclic) are a class of carcinogens that are important in these exposures. These compds. can be N- or O-acetylated by the NAT1 or NAT2 enzymes, resulting in activation or in some cases detoxification. Recent studies have shown that both NAT2 and NAT1 genes exhibit variation in human populations and that rapid acetylation by the NAT2 enzyme may be a risk factor for colorectal cancer. In this study the authors have analyzed for genetic polymorphism in both NAT1 and NAT2 in a group of 202 colorectal cancer patients and 112 control subjects from Staffordshire, England. The authors ***find*** significantly increased risk (odds ratio, 1.9;95% confidence interval, 1.2-3.2) assocd. with the NAT1*10 allele of NAT1, an allele that contains a variant ***polyadenylation*** ***signal*** . Individuals with higher stage tumors (Duke's C) were more likely to inherit this variant allele Z(odds ratio, 2.5; 95% confidence interval, 1.3-4.7). In contrast, rapid acetylation genotypes of NAT2 were not a

significant risk factor in this English population. However, the authors found that the risk assocd. with the NAT1 variant allele (NAT*10) was most apparent among NAT2 rapid acetylators (odds ratio, 2.8; 95% confidence interval, 1.4-5.7), suggesting a possible gene-gene interaction between NAT1 and NAT2 (test for interaction). This is the first study to test for cancer risk assocd. with the NAT1 gene, and these pos. ***findings*** suggest that NAT1 alleles may be important genetic determinants of colorectal cancer risk.

L5 ANSWER 75 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:742037 CAPLUS
DN 123:254107
TI Length polymorphism of the human complement component C4 gene is due to an ancient retroviral integration
AU Chu, Xiadon; Rittner, Christian; Schneider, Peter M.
CS Inst. Rechtsmedizin, Gutenberg Univ., Mainz, D-55131, Germany
SO Experimental and Clinical Immunogenetics (1995), 12(2), 74-81 CODEN: ECIME4; ISSN: 0254-9670
PB Karger
DT Journal
LA English
AB The fourth component of the complement system, C4, is encoded by two highly homologous MHC-linked genes expressing the two isotypes C4A and C4B. A gene size polymorphism (either 22.5 or 16 kb) has been described which depends on the presence or absence of a 6.5 kb insertion in intron 9 of the C4 gene. By sequencing a C4A-specific .lambda. clone from a human genomic library contg. the long intron 9 as well as PCR-amplified DNA contg. the short intron, the DNA sequences of both introns were detd. The long and short introns have lengths of 6,787 bp and 415 bp, resp. The sequence of the short intron is almost identical (96%) to the corresponding parts of the long intron. At position 282 of the short intron, a 6,372-bp insertion is present in the long intron which has all the characteristics of a full-length endogenous retrovirus. The proviral DNA is flanked by two 6-bp target site repeats. The orientation of the proviral sequence is opposite to that of the C4 coding strand. Long terminal repeats (LTRs) of 548 bp were found at both ends of the provirus. A TATA box and an SV40 enhancer core as well as a ***polyadenylation*** ***signal*** are present in the LTR. A 5' primer binding site for lysine tRNA was identified. The strongest sequence homologies were found in comparison to human endogenous retrovirus (HERV-K): between 65-88% for gag, pol and env genes. However, a ***search*** for open reading frames in these regions indicated the presence of multiple stop codons in all three reading frames. Thus it can be concluded that the retroviral genes are dysfunctional due to these mutations. It can be assumed that the integration of the retroviral sequence occurred prior to the sepn. of human and primate species, which can be dated to a period between 23 and 10 million years ago.

L5 ANSWER 76 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:731042 CAPLUS
DN 123:331381
TI Poly(A) addition site mapping and ***polyadenylation*** ***signal*** analysis in a plant circovirus replication-related gene
AU Merits, A.; Zelenina, D. A.; Mizenina, O. A.; Chernov, B. K.; Morozov, S. Yu.
CS A. N. Belozersky Inst. Physico-Chemical Biology, Moscow State Univ., Moscow, 119899, Russia
SO Virology (1995), 211(1), 345-9 CODEN: VIRLAX; ISSN: 0042-6822
PB Academic
DT Journal
LA English
AB The transcripts of a genomic component of coconut foliar decay virus (CFDV), a plant circovirus with a single-stranded DNA genome, were characterized by sequencing the 3' termini of the resp. cDNA clones. It was shown that transcription of the putative replication-related gene terminated at one major site (six bases downstream of the termination codon) in electroporated barley mesophyll protoplasts and that the resulting transcripts were polyadenylated. A deletion downstream of the AATAAA sequence including the poly(A) addn. site did not inhibit ***polyadenylation*** ***signal*** activity but altered the distance between the ***polyadenylation*** ***signal*** and the ***polyadenylation*** site. However, deletion of the sequences upstream of the AATAAA stretch resulted in inhibition of the polyadenylation in this region. These observations and the ***finding*** of a silent CFDV AATAAA sequence downstream of the active poly(A) signal confirm the role of the upstream elements in processing of RNA transcripts in plants.

L5 ANSWER 77 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:686439 CAPLUS
DN 124:1984
TI Molecular cloning and sequence analysis of Factor C cDNA from the Singapore horseshoe crab, Carcinoscorpius rotundicauda
AU Ding, Jeak L.; Navas, M. Anthony A., III; Ho, Bow
CS Marine Biotechnology Laboratory, National University Singapore, 0511, Singapore
SO Molecular Marine Biology and Biotechnology (1995), 4(1), 90-103 CODEN: MMBBEQ; ISSN: 1053-6426
PB Blackwell
DT Journal
LA English
AB Two forms of Factor C cDNAs: CrFC21 (3448 bp) and CrFC26 (4182 bp) were cloned into .lambda.gt22. CrFC26 includes 568 nucleotides of 5' untranslated region (5' UTR) contg. seven ATGs before the real initiation site, an open reading frame (ORF) of 3249 nucleotides, a stop codon, and 365 nucleotides of 3' untranslated sequence. There are 4 ***polyadenylation*** ***signals*** and 6 potential glycosylation sites. The ORF codes for a signal peptide of 24 amino acids and a Factor C zymogen of 1059 residues. The CrFC21 lacks most of the 5' UTR, and has some base changes in its ORF. The predicted secondary mRNA structures of the 5' end of CrFC26 showed numerous stem-and-loop structures, thus obscuring its real codon. In contrast, CrFC21 has a well-exposed AUG start site, and expresses Factor C in transcription-translation reactions in vitro. There is a typical serine protease catalytic triad of Asp-His-Ser, which is structurally like prothrombin, but catalytically more similar to trypsin. Although an overall homol. of 97.7% was obsd. in comparison with the Tachypleus tridentatus Factor C (TtFC) cDNA, there were notable differences in the restriction sites and subtle base substitutions in the CrFC cDNA. The high degree of homol. between Factor C from T. tridentatus and C. rotundicauda substantiates, at the mol. level, the proximity of these 2 species in the course of evolution. This ***finding*** contravenes the apparent disparities with respect to their morphol., ecol. habitat, and taxonomic classification.

L5 ANSWER 78 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:683625 CAPLUS
DN 123:102976
TI Cortisol up-regulates corticotropin releasing factor gene expression in the fetal ovine brainstem at 0.70 gestation
AU Keiger, C. Jane; O'Steen, W. Keith; Brewer, Gary; Sorci-Thomas, Mary; Zehnder, Timothy J.; Rose, James C.

CS Laboratory for Perinatal Research and Departments of Physiology and Pharmacology, Bowman Gray School of Medicine of Wake Forest University, Winston-Salem, NC, 27157-1083, USA
SO Molecular Brain Research (1995), 32(1), 75-81 CODEN: MBREE4; ISSN: 0169-328X
PB Elsevier
DT Journal
LA English
AB Glucocorticoids are important for the development of the central nervous system. In the ovine fetus, increased levels of plasma cortisol at term provide a stimulus to initiate parturition. CRF is central to this event in that it is one of the main modulators of the hypothalamic-pituitary- adrenal (HPA) axis. The purpose of the present study was to det. the effect of physiol. increases in fetal plasma cortisol levels on ACTH-releasing factor (CRF) gene expression in the developing ovine brain. Fetal plasma cortisol levels were chronically elevated at 0.70 gestation (100 days) to physiol. levels found at 0.90 gestation (130 days; term 145 days) when glucocorticoid-induced maturational changes are known to occur in the HPA axis. The 3' end of the ovine CRF gene encodes 4 putative ***polyadenylation*** (poly(A)) ***signals*** that may post-transcriptionally regulate gene expression through stability, translation and localization of the mRNA in a temporal and spatial manner. To det. whether CRF mRNA levels or poly(A) site usage are differentially regulated by cortisol in a region-specific manner, we used an RNase protection assay with an antisense CRF RNA probe from the 3' coding and untranslated regions of the gene to quantify changes in mRNA levels in the hypothalamus (Hypo), hippocampal-amygdala complex (H and A), frontal cerebral cortex (FCC) and brainstem. Our novel ***finding*** was a 3.5-fold increase in CRF mRNA levels in the medulla oblongata of fetuses from the cortisol group compared to those from the saline group. CRF mRNA levels in the Hypo, H and A and FCC did not change significantly in fetuses from the cortisol group. CRF mRNA transcripts derived from alternative poly(A) site usage were obsd. in all brain regions examd.; however, cortisol administration did not change the ratio of mRNAs polyadenylated at site 1 vs. sites 2-4. These results indicate that changes in the environment (e.g. physiol. increases in fetal plasma cortisol levels at an earlier time during development) have regional effects on CRF gene expression in the developing ovine brain.

L5 ANSWER 79 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:556039 CAPLUS
DN 123:277761
TI Identification and sequence analysis of the E1 genomic region of a porcine adenovirus
AU Kleiboeker, Steven B.
CS Virology Swine Research Unit, National Animal Disease Center, USDA, Agricultural Research Service, P.O. Box 70, 2300 Dayton Avenue, Ames, Iowa 50010, USA
SO Virus Research (1995), 36(2-3), 259-68 CODEN: VIREDF; ISSN: 0168-1702
PB Elsevier
DT Journal
LA English
AB The complete nucleotide sequence of the putative early transcriptional region 1 (E1) of the genome of NADC-1, a porcine adenovirus, was detd. The E1 region of NADC-1 was 3658 bp and located between 0 and 11.2 map units. Twelve potential open reading frames (ORFs) and 5 ***polyadenylation*** ***signals*** were identified in the r strand. The nucleotide sequence and each predicted amino acid sequence were compared to sequences available on a no. of databases by a BLAST ***search*** and comparison. A single region of nucleotide sequence similarity was identified with the sequence of human adenovirus 5. Only 2 of the 12 potential ORFs encode polypeptides that have homol. to known adenovirus polypeptides. For these predicted proteins, similarities were found with a no. of adenovirus proteins. The strongest homol. was found to potential E1 products of bovine adenovirus 3.

L5 ANSWER 80 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:483106 CAPLUS
DN 122:237016
TI Deletion of the C-terminal end of aspartylglucosaminidase resulting in a lysosomal accumulation disease: evidence for a unique genomic rearrangement
AU Jalanko, Anu; Manninen, Tuula; Peltonen, Leena
CS Dep. Human Mol. Genetics, Natl. Public Health Institute, Helsinki, FIN-00300, Finland
SO Human Molecular Genetics (1995), 4(3), 435-41 CODEN: HMGEE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
AB Aspartylglucosaminuria (AGU) is an inborn error of glycoprotein catabolism and represents the only known human deficiency of an amidase, aspartylglucosaminidase (AGA, EC 3.5.1.26). We report here a detailed characterization of a unique 2 kb deletion of the AGA gene in a North American AGU patient. To facilitate the characterization of the deletion, genomic lambda clones spanning the 3' flanking region of human AGA were isolated and sequenced. The breakpoint of the deletion was detd. from the patient's DNA by sequencing the genomic region contg. the novel junction. The rearrangement involved a nonhomologous recombination with only 2 bp of homol. at the deletion breakpoint. The deletion's 5' breakpoint was located in the last intron of AGA, thus abolishing the normal C-terminal exon. This is in contrast to our previous ***findings*** indicating that the deletion in the AGA gene would contain only the complete 3' untranslated region and leave the coding region intact (1). The unique feature of this deletion is a triplication of 19 thymidine nucleotides of an inverted Alu repeat, which is located at the deletion 3' breakpoint. The anal. of the patient's AGA cDNA revealed an open reading frame contg. a novel C-terminal exon, coding for a 64 amino acid sequence, which has no homol. to the normal exon 9 of AGA. This new exon has a functional splice acceptor site at its 5' end, a stop codon, and a ***polyadenylation*** ***signal*** at the 3' end. Expression of the mutant AGA cDNA in COS cells showed that mutant mRNA is synthesized in equal amts. compared with normal. However, the mutant polypeptide precursor is not processed into the mature subunits of AGA, and is totally degraded within 24 h of synthesis.

L5 ANSWER 81 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:475227 CAPLUS
DN 123:163483
TI Expression of Hox A11 in the limb and the regeneration blastema of adult newt
AU Beauchemin, Michel; Noiseux, Nicolas; Tremblay, Monique; Savard, Pierre
CS Centre de Recherches, Universite Laval, Quebec, QC, G1V 4G2, Can.
SO International Journal of Developmental Biology (1994), 38(4), 641-9 CODEN: IJDBE5; ISSN: 0214-6282
DT Journal
LA English
AB Homeoproteins are functionally involved in pattern formation of developing systems and are potentially good candidates to regulate positional information during limb regeneration in the newt. Here the authors report the mol. structure of Hox A11 and its pattern of expression during the regeneration of adult newt

appendages. The transcriptional unit of the gene is composed of two exons sepd. by an intron. Northern blots revealed two major transcripts; a size difference would result from using two different ***polyadenylation*** ***signals*** . Therefore, the gene would encode a single protein that is very homologous to other vertebrate counterparts. The pattern of expression of Hox A11 in the adult newt shows interesting ***findings*** in relation to limb regeneration. First, expression is found in both intact limb and tail, showing maintenance of expression of an important regulator of development in the appendages of the adult newt. Second, Hox A11 is expressed mainly in the muscle and the bone of intact limbs, two tissue fractions known to participate in blastemal fate detn. Third, the level of Hox A11 expression increases drastically in both limb and tail regeneration blastemas, suggesting that the population of expressing cells is preferentially recruited during blastema formation. Finally, proximal blastemas (mid-humerus) significantly express higher levels of transcript compared with distal ones (mid-radius and ulna). These features of expression suggest that Hox A11 may participate in limb pattern formation by specifying positional information to the progenitor cells of the regenerate.

L5 ANSWER 82 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:457762 CAPLUS
DN 123:76341
TI Characterization of the proximal promoter of the human histone H2A.Z gene
AU Hatch, Christopher L.; Bonner, William M.
CS Natl. Cancer Inst., Natl. Inst. of Health, Bethesda, MD, 20892, USA
SO DNA and Cell Biology (1995), 14(3), 257-66 CODEN: DCEBE8; ISSN: 1044-5498
PB Liebert
DT Journal
LA English
AB Histone H2A.Z is a distinct and evolutionarily conserved member of the histone H2A family whose synthesis, in contrast to that of most other histone species, is not dependent on DNA replication. The gene for H2A.Z lacks the signals involved in the 3' processing of replication-linked histone mRNA species and contains introns as well as ***polyadenylation*** ***signals*** . The H2A.Z gene proximal promoter, a 200-bp region upstream of the transcription start site that provides maximal activity in CAT reporter studies, contains three CCAAT and two GGGCGG elements as well as a consensus TATA element. In vitro DNase I footprint anal. of this region indicated that the central CCAAT and the distal GGGCGG elements were protected by factors present in HeLa nuclear ext. Site-directed mutations of selected promoter elements were generated in the H2A.Z gene promoter region of a CAT reporter construct by a novel one-step PCR procedure. Of the elements examd., the central CCAAT element was found to be the most important determinant of promoter activity; its disruption decreased CAT reporter activity by 65%. Disruption of the proximal CCAAT or the distal GGGCGG elements led to decreases in activity of 40%, while disruption of any of the other examd. led to smaller decreases. Gel-mobility shift anal. showed that the three CCAAT elements had overlapping but not identical binding specificities for nuclear factors. The two GGGCGG elements both were found to bind transcription factor Sp1, but the distal element bound Sp1 with higher affinity. The ***findings*** show that the central and proximal CCAAT elements and the distal GGGCGG element appear to be the major determinants of the transcriptional activity of the H2A.Z gene.

L5 ANSWER 83 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:451337 CAPLUS
DN 123:248230
TI Molecular cloning and nucleotide sequence of the coat protein gene from garlic mosaic virus
AU Fan, Yougjian; Wu, Shuhua; Lu, Zhenxiao; Xu, Zhengkai
CS Institute of Plant Protection, Jiangsu Academy of Agricultural Sciences, Nanjing, 210014, Peop. Rep. China
SO Zhongguo Bingduxue (1994), 9(4), 333-40 CODEN: ZBINER; ISSN: 1003-5125
PB Kexue
DT Journal
LA Chinese
AB The authors have isolated garlic mosaic virus (GarMV) from naturally infected garlic plants and synthesized various partial cDNA fragments using the GarMV genomic RNA as template. The length of the coat protein (CP) gene was estd. about 0.8.apprx.0.9 kb based on the estd. mol. wt. of the coat protein subunit by protein SDS-polyacrylamide gel anal. Several clones contg. cDNA fragments larger than 2kb were ***searched*** for a 3' terminal cDNA fragment including the complete CP gene and noncoding region. One clone, pGM495 contg. a 2.4kb fragment was identified to be related to GarMV genomic RNA by Northern blotting assay and to contain the 3'-terminal poly(A) tract by terminal sequencing anal. suggesting the presence of these regions. The cDNA fragment in pGM495 has been completely sequenced. It contains 2379bp and three unique restriction sites, EcoRI, PstI and BamHI, which are consistent with the primary restriction endonuclease mapping anal. There are several in-frame stop codons, the first stop codon TAA is located at the position 264 upstream from the 3' end. By comparison with the known sequences of the CP genes and the proteolytic cleavage sites for coat protein subunits from other potyviruses, the authors have deduced that the CP gene of GarMV encodes 302 amino acids, starting at the position 1170 bp upstream from the 3'-terminus, with a calcd. mol. wt. of 36 kDa which is slightly larger than that estd. by SDS-PAGE anal. The 3'-terminal noncoding region (264 bp) is AT-rich. A putative ***polyadenylation*** ***signal*** site AATAAA is located at the position 27.apprx.32 from the 3' terminus.

L5 ANSWER 84 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:450922 CAPLUS
DN 123:49129
TI Transcriptional analyses of the unique short segment of EHV-1 strain Kentucky A genome
AU Colle, Clarence F., III; O'Callaghan, Dennis J.
CS Med. Cent., Louisiana State Univ., Shreveport, LA, USA
SO Virus Genes (1995), 9(3), 257-68 CODEN: VIGEET; ISSN: 0920-8569
PB Kluwer
DT Journal
LA English
AB The unique short (Us) segment of the genome of equine herpesvirus type 1 (EHV-1) strain KyA is comprised of six open reading frames (ORFs) that encode: (a) a homolog of the Us2 protein of herpes simplex virus type 1 (HSV-1); (b) a serine threonine protein kinase that is a homolog of the HSV-1 US3 protein; (c) a homolog of pseudorabies virus glycoprotein gX and HSV-2 gG; (d) a novel glycoprotein, EUS4, not encoded by other herpesviruses sequenced to date; (e) a homolog of HSV-1 gD; and (f) a homolog of HSV-1 Us9. The KyA strain is a deletion mutant that lacks Us sequences encoding gI, gE, and a potential 10 kD polypeptide, and thus may be useful as a parent virus for the generation of live virus vaccines. To complete the elucidation of the transcriptional program of the Us segment, Northern blot hybridization and S1 nuclease anal. were performed on poly(A)+-selected RNA isolated from infected cells maintained under early (phosphonoacetic acid-block) and late conditions. The ***findings*** revealed that the gene (EUS ORF) encoding the

protein kinase es expressed as an early 2.9 kb transcript that overlaps nd is 3' coterminal with a 1.6 kb and 5.8 kb are 5' coterminal and may both encode the novel glycoprotein gene EUS4. The 1.6 kb transcript terminates at a poly(A) signal site downstream of the EUS4 ORF, and the 5.i kb transcript terminates within the inverted repeat (IR) segment. Overall, the transcriptional program of the EHV-1 KyA Us segment is complex and exhibits similarities to that of HSV-1 US segment: (a) transcripts arise from both DNA Strands; (b) some transcripts, including those mapping at the termini of the Us segment, extend into the IR segments and are 3' coterminal with the 1.2 kb IR6 transcript; (c) at least one transcript reads through a functional ***polyadenylation*** ***signal*** ; (d) some transcripts encoding genes that lie in different reading frames exist as a family of overlapping mRNAs, come in an anti-sense manner. Lastly, of the six US genes of the EHV-1 KyA strain, only those encoding the EHV-1 protein kinase and the HSV-2 gG/gX homolog are members of the early kinetic class.

L5 ANSWER 85 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:379120 CAPLUS
DN 123:76082
TI The human gonadotropin-releasing hormone receptor gene: complete structure including multiple promoters, transcription initiation sites, and ***polyadenylation*** ***signals***
AU Fan, Nancy C.; Peng, Chun; Krisinger, John; Leung, Peter C. K.
CS Dep. Obstetrics and Gynaecology, Univ. British Columbia, Vancouver, BC, V6H 3V5, Can.
SO Molecular and Cellular Endocrinology (1994), 107(2), R1-R8 CODEN: MCEND6; ISSN: 0303-7207
PB Elsevier
DT Journal
LA English
AB The interaction of gonadotropin-releasing hormone and its receptor is a crit. event in the endocrine regulation of reprodn. The authors have recently cloned the gene encoding for the human gonadotropin-releasing hormone receptor (hGnRHR). Partial sequence anal. revealed a structural organization consisting of three exons and two introns. Exon II contains only 219 bp and the remainder of the approx. 5 kb transcript is distributed between exons I and III. The complete coding region for the hGnRHR represented only 987 bp leaving an extensive 5' and 3' non-translated region and potentially addnl. exons unaccounted for. This report provides the complete sequence of exon I and III and demonstrates that further exons are unlikely to be contained within this gene. Sequencing of the 5' end of the gene revealed the presence of five consensus TATA sequences distributed within a 700 nucleotide region. Primer extension anal. detected multiple transcription initiation sites assocd. with this cluster of TATA sequences. Transcription of this region up to the most 5' initiation site was demonstrated by the reverse transcription-polymerase chain reaction (RT-PCR) method. The 5' non-translated region stretches between 703 and 1393 bp, depending on which initiation site is used. Several consensus cis-acting regulatory sequences were identified within the 5' end. These include, among others, sites for PEA-3, AP-1, and Pit-1. In addn., cAMP response element (CRE)-like and glucocorticoid/progesterone response element (GRE/PRE)-like sequences were found. The 3' end of the gene was also sequenced and five classical ***polyadenylation*** ***signals*** were found scattered over a region of 800 nucleotides. PT-PCR conducted on the 3' non-translated region confirmed transcription up to the fifth ***polyadenylation*** ***signal*** . Factoring in the location of the most 5' initiation site and the most 3' ***polyadenylation*** ***signal*** , the total transcript covers a region of 5499 bp. The ***finding*** of multiple transcription initiation sites and ***polyadenylation*** ***signals*** raises the possibility of tissue-specific regulation and the existence of variable transcripts for the hGnRHR. The presence of a CRE-like sequence, Pit-1 binding site, and a GRE/PRE-like sequence is consistent with the notion that cAMP, Pit-1, and progesterone are candidates for controlling the expression of this key receptor in reproductive physiol.

L5 ANSWER 86 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1994:526768 CAPLUS
DN 121:126768
TI RNA 3' end signals of the S. pombe ura4 gene comprise a site determining and efficiency element
AU Humphrey, Tim; Birse, Charles E.; Proudfoot, Nick J.
CS Sir William Dunn Sch. Pathol., Oxford Univ., Oxford, OX1 3RE, UK
SO EMBO Journal (1994), 13(10), 2441-51 CODEN: EMJODG; ISSN: 0261-4189
DT Journal
LA English
AB The authors have defined sequences in the 3' non-coding region of the Schizosaccharomyces pombe ura4 gene that are required for efficient mRNA 3' end formation. Three sep. sequence elements have been identified. Two of these are site detg. elements which specify alternative sites of polyadenylation [the major poly(A) site and a minor downstream poly(A) site]. The third sequence, located downstream of both poly(A) sites, functions as an efficiency element that enhances utilization of either polyadenylation site. By employing sensitive RT-PCR anal., the authors demonstrate that although low levels of transcripts are detected up to the efficiency element, none is detected beyond this point. The downstream site detg. element and efficiency element have both been delineated to specific 16 nt sequences which the authors show are together sufficient for ura4 mRNA 3' end formation. The authors have further characterized the interaction between these two elements and show that the efficiency element behaves in a position-independent, orientation-dependent manner, but cannot form 3' ends independently of the site detg. element. Surprisingly, the authors ***find*** that the efficiency element can be functionally replaced by a second copy of either site detg. element. The authors present a model for the mechanism of RNA 3' end formation of the ura4 gene and note that this bipartite structure for a poly(A) signal in S. pombe may be related to the AAUAAA and downstream GU-rich sequences of poly(A) signals in mammalian genes.

L5 ANSWER 87 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1994:500998 CAPLUS
DN 121:100998
TI Structure of the mouse gonadotropin-releasing hormone receptor gene: variant transcripts generated by alternative processing
AU Zhou, Wei; Sealfon, Stuart C.
CS Fishberg Research Center for Neurobiology, Mount Sinai Medical Center, New York, NY, 10029, USA
SO DNA and Cell Biology (1994), 13(6), 605-614 CODEN: DCEBE8; ISSN: 1044-5498
DT Journal
LA English
AB The mouse gonadotropin-releasing hormone receptor (GnRHR) is unique among G-protein-coupled receptors in its lack of a putative intracellular carboxy-terminal domain. A gonadotrope cell line cDNA library was screened in a ***search*** for alternative forms of the receptor transcript and 42 clones were obtained, representing a no. of variant cDNAs. To det. the origin of these transcripts, the structure of the mouse

gene was mapped from 11 distinct genomic clones. The gene contains three exons, spanning more than 22 kb. Exons 1, 2, and 3 encode, resp., nucleotides +1 to +522, +523 to +739, and +740 to +981 of the open reading frame of the cDNA for the functional mouse GnRHR. Southern blot anal. with genomic DNA is consistent with the presence of a single gene. By comparison with the genomic sequence, the origins of the variant cDNAs isolated can be clarified. All the cDNAs contain the first exon and the majority (71%) encode the functional 327-amino-acid receptor previously reported. One group of clones (14%), which contains exons 1 and 2, continues 700 bp past the exon 2 splice donor of the wild-type receptor. These clones terminate after a ***polyadenylation*** ***signal*** and have an open reading frame encoding a protein of only 261 amino acids. In a different group of transcripts (5%), exon 2 is absent, resulting in a shift in the reading frame and encoding a protein of 177 amino acids. These data support alternative processing of the mouse GnRHR gene.

L5 ANSWER 88 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1994:474870 CAPLUS
DN 121:74870
TI Nucleotide sequence of the genomic region encompassing Adh and Adh-Dup genes of D. lebanonensis (Scaptodrosophila): gene expression and evolutionary relationships
AU Juan, Elvira; Papaceit, M.; Quintana, A.
CS Dep. Genet., Univ. Barcelona, Barcelona, 08071, Spain
SO Journal of Molecular Evolution (1994), 38(5), 455-67 CODEN: JMEVAU; ISSN: 0022-2844
DT Journal
LA English
AB The region of the genome of D. lebanonensis that contains the Adh gene and the downstream Adh-dup gene was sequenced. The structure of the 2 genes is the same as has been described for D. melanogaster. Adh has 2 promoters and Adh-dup has only one putative promoter. The levels of expression of the 2 genes in this species are dramatically different. Hybridizing the same Northern blots with a specific probe for Adh-dup, the authors did not ***find*** transcripts for this gene in D. lebanonensis. The level of Adh distal transcript in adults of D. lebanonensis is 5 times greater than that of D. melanogaster adults. The max. levels of proximal transcript are attained at different larval stages in the 2 species, being 3 times higher in D. melanogaster late-second-instar larvae than in D. lebanonensis first-instar larvae. The level of Adh transcripts allowed the authors to det. distal and proximal initiation transcription sites, the position of the first intron, the use of 2 ***polyadenylation*** ***signals*** , and the heterogeneity of polyadenylation sites. Temporal and spatial expression profiles of the Adh gene of D. lebanonensis show qual. differences compared with D. melanogaster. Adh and Adh-dup evolve differentially as shown by the synonymous and nonsynonymous substitution rates for the coding region of both genes when compared across 2 species of the melanogaster group, two of the obscura group of the subgenus Sophophora and D. lebanonensis of the victoria group of the subgenus Scaptodrosophila. Synonymous rates for Adh are approx. half those for Adh-dup, while nonsynonymous rates for Adh are generally higher than those for Adh-dup. Adh shows 76.8% identities at the protein level and 70.2% identities at the nucleotides at the nucleotide level while Adh-dup shows 83.7% identities at the protein level and 67.5% identities at the nucleotide level. Codon usage for Adh-dup is shown to be less biased than for Adh, which could explain the higher synonymous rates and the generally lower nonsynonymous substitution rates in Adh-dup compared with Adh. Phylogenetic trees reconstructed by distance matrix and parsimony methods show that Sophophora and Scaptodrosophila subgenera diverged shortly after the sepn. from the Drosophila subgenus.

L5 ANSWER 89 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1994:262486 CAPLUS
DN 120:262486
TI Nucleotide sequences of a soybean complementary DNA encoding a 50-kilodalton late embryogenesis abundant protein
AU Hsing, Yue Ie C.; Chen, Zuei Ying; Chow, Teh Yuan
CS Inst. Bot., Acad. Sin., Taipei, Taiwan
SO Plant Physiology (1992), 99(1), 354-5 CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
AB The sequence of a cDNA clone, pGmPM2, corresponding to a soybean mature seed-abundant mRNA (GmPM2) is reported. Only 1 long open reading frame was found, and the mol. wt. of the deduced protein was similar to that predicted by hybrid select translation. The deduced protein is very hydrophilic, and consists of 463 amino acid (aa) residues corresponding to a mol. mass of 50.6 kD. One potential ***polyadenylation*** ***signal*** , AATAAA, is in the 3'-noncoding region, 102 nt upstream from the poly(A+) tail. A ***search*** for polypeptide homologies in data banks revealed a strong local similarity with several Lea proteins, including embryonic protein DC8 in carrot, Lea proteins D7 and D29 in cotton, ABA-induced protein PHVA1 in barley, and Lea protein 76 in rape. Another protein with strong local similarity is the Plasmodium falciparum S antigen present in the sera of some malaria-infected individuals. All of these proteins are sol. heat-stable proteins with a series of tandemly repeated aa domains, and most of these proteins have no Trp or Cys residues.

L5 ANSWER 90 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1994:209784 CAPLUS
DN 120:209784
TI B94, a primary response gene inducible by tumor necrosis factor-.alpha., is expressed in developing hematopoietic tissues and the sperm acrosome
AU Wolf, Frederick W.; Sarma, Vidya; Seldin, Michael; Drake, Sandra; Suchard, Suzanne J.; Shao, Haining; O'Shea, K. Sue; Dixit, Vishva M.
CS Med. Sch., Univ. Michigan, Ann Arbor, MI, 48109, USA
SO Journal of Biological Chemistry (1994), 269(5), 3633-40 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB B94 was originally described as a novel tumor necrosis factor-.alpha.-inducible primary response gene in endothelial cells which was also induced in an in vitro model of angiogenesis. To further characterize its expression, the authors cloned the mouse homolog and mapped its developmental and tissue specific expression. The predicted amino acid sequence of mouse B94 was found to be 83% similar to its human homolog. The gene was localized to mouse chromosome 12 just centromeric to the Ig heavy chain locus, in a region that is often rearranged in T-cell neoplasms. To explore the possibility that B94 is expressed during vasculogenesis and other developmental processes, the expression of its transcript was detd. during mouse development by in situ hybridization. In 10-day embryos B94 was expressed prominently in the myocardium and in the aortic arch. By the 15th day of gestation, expression was restricted largely to the liver, the bone forming regions of the jaw, the aortic endothelium, and the nasopharynx: a pattern that was maintained until just prior to birth. Postnatally, expression shifted to the red pulp of the spleen and the thymic medulla. B94 expression was extinguished in most adult tissues but was detectable in lymphopoietic tissues including the spleen, tonsil,

and lymphatic aggregates in the gut. Consistent with this was the ***finding*** that mononuclear progenitor cells in bone marrow and mature peripheral blood monocytes expressed B94. A truncated testis-specific transcript previously identified by Northern blot anal. was detd. to result from the use of an alternate ***polyadenylation*** ***signal*** which was surprisingly located with the open reading frame. This shorter transcript was expressed at high levels exclusively in late stage spermatids. Immunostaining with an affinity-purified polyclonal antiserum revealed B94 to be localized to the acrosomal compartment of mature sperm. These studies demonstrate that B94 expression is tightly regulated during development and suggests distinct roles for B94 in myelopoiesis and spermatogenesis.

L5 ANSWER 91 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1994:188647 CAPLUS
DN 120:188647
TI Characterization of nondeletion .alpha.-thalassemia mutations in the Greek population
AU Traeger-Synodinos, Joanne; Kanavakis, Emmanuel; Tzetis, Maria; Kattamis, Antonios; Kattamis, Christos
CS 1st Dep. Pediatr., Athens Univ., Athens, Greece
SO American Journal of Hematology (1993), 44(3), 162-7
CODEN: AJHEDD; ISSN: 0361-8609
DT Journal
LA English
AB .alpha.-Thalassemia is usually due to deletions within the .alpha.-globin gene cluster, leading to loss of function of one (-.alpha.) or both [-(.alpha.) or --] .alpha.-globin genes. Non-deletion mutations (denoted .alpha..alpha.T or .alpha.T.alpha.) are less frequent and in Greece are not well defined. The authors report the anal. of 16 non-deletion .alpha.-thalassemia chromosomes using a polymerase chain reaction method to amplify specifically the .alpha.2-globin gene, which was subsequently screened using ASO hybridization or restriction enzyme anal. for four mutations already characterized in other Mediterranean and Middle Eastern populations. Of the 16 non-deletion chromosomes, nine had the ***polyadenylation*** ***signal*** mutation (.alpha.PolyA.alpha.), two the IVSI 5' pentanucleotide deletion (.alpha.Hph.alpha.), two the Hb Icaria mutation (.alpha.Ic.alpha.), and one the initiation codon mutation (.alpha.Nco.alpha.). In two, the defects are still undefined. These ***findings*** show that non-deletion .alpha.-thalassemia in Greece is heterogeneous and that the most frequent mutation (accounting for >50%) is the ***polyadenylation*** ***signal*** mutation, which to date was most commonly found in the Saudi Arabian population.

L5 ANSWER 92 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1994:153103 CAPLUS
DN 120:153103
TI Characterization of a DNA topoisomerase II.alpha. gene rearrangement in Adriamycin-resistant P388 leukemia: Expression of a fusion messenger RNA transcript encoding topoisomerase II.alpha. and the retinoic acid receptor .alpha. locus
AU McPherson, J. Peter; Brown, Greg A.; Goldenberg, Gerald J.
CS Dep. Pharmacol., Univ. Toronto, Toronto, ON, M5G 1L4, Can.
SO Cancer Research (1993), 53(24), 5885-9 CODEN: CNREA8; ISSN: 0008-5472
DT Journal
LA English
AB Previous studies using cloned lines of Adriamycin-sensitive and -resistant P388 murine leukemia cells have suggested that a redn. in DNA topoisomerase II.alpha. (topo II.alpha.) enzyme activity and protein levels in drug-resistant cell lines may be due to an allelic mutation in the topo II.alpha. gene (A. M. Deffie, et al., 1989). The drug-resistant cell lines P388/ADR/3 and P388/ADR/7 express a shortened topo II.alpha. mRNA transcript in addn. to the native transcript present in the drug-sensitive P388/4 cell line. Using complementary DNA probes derived from the coding sequence and 3' untranslated region of the native mouse topo II.alpha. transcript, the authors have detd. that the shorter 4.5-kilobase topo IIK.alpha. transcript expressed in the drug-resistant cell lines contains only 3.5-kilobases of topo II sequence from the 5'-terminus onwards. Using a 3'-rapid amplification of cDNA ends strategy, the authors have cloned cDNAs representing the 3'-termini of both the native and mutant transcripts from both P388/ADR/3 and P388/ADR/7 cells. DNA sequence anal. revealed that the shorter 4.5-kilobase transcript: (a) encodes topoisomerase II.alpha. unit nucleotide position 3494, at which point the sequence diverges for the remaining 956 bases; (b) contains a ***polyadenylation*** ***signal*** distinct from the native transcript; and (c) contains an open reading frame predicting a truncated topo II.alpha. fusion protein. Of great interest was the ***finding*** that the non-topo II.alpha. 956-base sequence in the shorter transcript encodes the promoter, exon I, and part of the first intron of the murine retinoic acid receptor .alpha. gene locus in the antisense orientation, suggesting that a rearrangement on chromosome 11 in the drug-resistant cells led to a gene fusion event between the loci encoding topo 11.alpha. and retinoic acid receptor .alpha..

L5 ANSWER 93 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:642383 CAPLUS
DN 119:242383
TI Characterization and genetic organization of full-length copies of a LINE retroposon family dispersed in the genome of Culex pipiens mosquitoes
AU Agarwal, Munna; Bensaadi, Nacira; Salvado, Jean Claude; Campbell, Keith; Mouches, Claude
CS Lab. Ecol. Mol., Univ. Pau Pays de l'Adour, Pau, 64000, Fr.
SO Insect Biochemistry and Molecular Biology (1993), 23(5), 621-9 CODEN: IBMBES; ISSN: 0965-1748
DT Journal
LA English
AB Many full-length copies of a long interspersed repetitive element family, designated Juan-C, are reiterated in the genome of Culex pipiens mosquitoes. The complete Juan-C elements have a length of 4.48 kb. They are terminated at one end with an adenosine-rich sequence preceded with an AATAAA ***polyadenylation*** ***signal*** , lack terminal repeats and cause duplication of the host DNA at the site of their integration. Full-length Juan-C copies display two long open reading frames potentially encoding two proteins. The first one includes a domain typical of nucleic-acid-binding proteins, while the second resembles reverse transcriptases. Therefore, Juan-C elements are similar to LINE retroposons in their overall genetic organization and can probably be transposed by reverse transcription of an RNA intermediate. Juan-C elements are most similar in their sequence and coding potential to the Juan-A elements which are reiterated in mosquito species belonging to the genus Aedes. They also display homologies with some Drosophila LINEs such as Jockey, suggesting that all these elements have arisen from a common precursor. Nearly identical full-length Juan-C copies are amplified in C. pipiens strains from different continents. This ***finding*** that Juan-C retroposons reiterated in different strains form a homogeneous family is interpreted to indicate that these elements have spread recently in the C. pipiens species.

L5 ANSWER 94 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:623205 CAPLUS
DN 119:223205

TI A mutation in the 3' untranslated region of the factor IX gene in four families with hemophilia B
AU Vielhaber, Erica; Jacobson, David P.; Ketterling, Rhett P.; Liu, Jing Zhong; Sommer, Steve S.
CS Dep. Biochem. Mol. Biol., Mayo Clin. Found., Rochester, MN, 55905, USA
SO Human Molecular Genetics (1993), 2(8), 1309-10 CODEN: HMGEE5; ISSN: 0964-6906
DT Journal
LA English
AB Hemophilia B is an X-linked coagulopathy caused by defects in the factor IX gene. The authors have examd. the putative promoter region, the coding sequence, and splice junctions in 320 consecutive families with hemophilia B. Mutations have been found in all but 18 of these families (94%). In the ***search*** for the undefined mutations in these 18 cases, the region adjacent to the polyadenylation site was sequenced. In four families an A to G transition was detected at base pair 32, 528, 208 bp 5' of the ***polyadenylation*** ***signal*** . This transition creates a potential splice donor site in the 3' untranslated region of the factor IX gene. The affected individuals have clin. severe disease assocd. with factor IX coagulants of less than 3%, and factor IX antigens of less than 1%. Haplotype analyses suggest that the mutation occurred independently at least three times.

L5 ANSWER 95 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:576133 CAPLUS
DN 119:176133
TI Nucleotide sequence of a cDNA encoding a pathogenesis-related protein, P1-p14, from tomato (Lycopersicon esculentum)
AU Tornero, Pablo; Rodrigo, Ismael; Conejero, Vicente; Vera, Pablo
CS Dep. Biotecnologia, Univ. Politec. Valencia, Valencia, 46022, Spain
SO Plant Physiology (1993), 102(1), 325 CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
AB The sequence of a cDNA clone, pTE 28.1, corresponding to a tomato (Lycopersicon esculentum) pathogenesis-related protein mRNA is reported. It was selected from an ethylene-treated tomato leaf cDNA .lambda.ZAP II library screened by differential hybridization with single-stranded cDNA probes prepd. from untreated and ethylene-treated leaf poly(A+) RNA. The pTE 28.1 cDNA clone is 711 bp long. The open reading frame encodes a precursor protein of 159 amino acids, and the mol. mass of the deduced protein is similar to that predicted by in vitro translation-immunopptn. expts. The first 24 amino acids represent a signal peptide that is processed to render the mature protein. The deduced protein sequence from the pTE 28.1 cDNA contains five addnl. amino acid residues (Trp-Arg-Asn-Ser-Val) positioned between amino acid 97 and 98 of the published sequence of p14 obtained by direct protein sequencing (Lucas, I. et al., 1985). Three potential ***polyadenylation*** ***signals*** are found in the 3' noncoding region. A ***search*** for homologies in data banks revealed coincidence with a cDNA clone (P6) isolated from fungi-infected tomato leaves, but the pTE 28.1 clone obtained extends 25 more nucleotides in the 5' end. Clone pTE 28.1 also shows similarities with counterpart pathogenesis-related genes from tobacco.

L5 ANSWER 96 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:487777 CAPLUS
DN 119:87777
TI A human endogenous long terminal repeat provides a ***polyadenylation*** ***signal*** to a novel, alternatively spliced transcript in normal placenta
AU Goodchild, Nancy L.; Wilkinson, David A.; Mager, Dixie L.
CS Terry Fox Lab., BC Cancer Agency, Vancouver, BC, V5Z 1L3, Can.
SO Gene (1992), 121(2), 287-94 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB The authors have been investigating the impact that the long terminal repeats (LTRs) of the RTVL-H family of human endogenous retroviral-like elements may have on the expression of adjacent cellular genes. Using a differential hybridization strategy, the authors have screened a cDNA library from a normal full-term human placenta and have identified 2 clones contg. non-RTVL-H-related cellular sequences that have been polyadenylated within an RTVL-H LTR. One of these clones, cPj-LTR, contains an opening reading frame (ORF) of 223 amino acids. Southern anal. indicated that the corresponding gene, termed PLT, is most probably a single multi-exon locus and that related sequences are present in the mouse genome, suggesting that this gene has been evolutionarily conserved. Database ***searches*** detected no significant homol. to previously published sequences, indicating that PLT is a novel gene. Northern anal. identified several PLT-related transcripts in placental RNA sampales, 1 of which is assocd. with the LTR. The presence of this PLT-LTR fusion transcript in normal placenta was also confirmed by PCR. Addnl. hybridization studies with RNAs from various cell lines suggested that the PLT locus is differentially expressed in different cell types. To investigate the structure of the non-LTR-assocd. PLT-related transcripts, addnl. clones were isolated from the placental cDNA library. Anal. of these clones suggests that the PLT mRNA undergoes alternative splicing at its 3' end, with polyadenylation within an RTVL-H LTR occurring in 1 of the resulting transcripts.

L5 ANSWER 97 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:442553 CAPLUS
DN 119:42553
TI Blepharisma uses UAA as a termination codon
AU Liang, A.; Heckmann, K.
CS Inst. Allg. Zool. Genet., Univ. Muenster, Muenster, W-4400, Germany
SO Naturwissenschaften (1993), 80(5), 225-6 CODEN: NATWAY; ISSN: 0028-1042
DT Journal
LA English
AB Here, it is reported that, similar to Euplotes, the heterotrichous ciliate Blepharisma uses UAA as a termination codon and not for encoding glutamine. The .alpha.-tubulin gene of B. japonicum terminates with a TAA. Another nonidentified gene also ends with a TAA. The last amino acid derived from the cloned cDNA of the .alpha.-tubulin of B. japonicum is a leucine residue. In most eukaryotes .alpha.-tubulin ends with a tyrosine. In the Blepharisma cDNA an AATAAA sequence was found 4 bp downstream of the termination codon. The sequence may act as a ***polyadenylation*** ***signal*** . The ***finding*** that UAA is used as a stop codon not only in Euplotes but also in Blepharisma makes clear that the unusual code found in Paramecium, Tetrahymena, Stylonychia, and Oxytricha was not employed in the phylum Ciliophora from the beginning but must have evolved after the ciliates had sepd. from the main eukaryote line. It is not clear whether UAA is the only stop codon used by Blepharisma.

L5 ANSWER 98 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN

AN 1993:442437 CAPLUS
DN 119:42437
TI Characterization of seven processed pseudogenes of nucleophosmin/B23 in the human genome
AU Liu, Qing Rong; Chan, Pui K.
CS Dep. Pharmacol., Baylor Coll. Med., Houston, TX, 77030, USA
SO DNA and Cell Biology (1993), 12(2), 149-56 CODEN: DCEBE8; ISSN: 1044-5498
DT Journal
LA English
AB Genomic blot anal. revealed that the nucleophosmin/B23 gene belongs to a multigene family that has about 10 copies per haploid human genome. In ***searching*** for human nucleophosmin/B23 functional genes, 7 processed pseudogenes (NG1-1.6, NG2-6, NG3-3, NG4-5, NG5-4, NG6-4, and NG7-6) were isolated and characterized. Four of them, NG2-6, NG3-3, NG4-5, and NG7-6, contain the sequences corresponding to the full-length cDNA. NG1-1.6 is 5'-truncated, whereas NG5-4 and NG6-5 are 3'-truncated pseudogenes. Of the 7 pseudogenes, the NG3-3 clone has the longest 5' untranslated sequence, which contains 104 nucleotides upstream of the translation initiation codon (AUG). Two processed pseudogenes (NG2-6 and NG3-3) have different polyadenylation sites from the mRNA, indicating the usage of alternative ***polyadenylation*** ***signals*** at the 3' sequence.

L5 ANSWER 99 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:421641 CAPLUS
DN 119:21641
TI cDNA cloning and chromosome assignment of the gene for human brain 14-3-3 protein .eta. chain
AU Ichimura-Ohshima, Y.; Morii, K.; Ichimura, T.; Araki, K.; Takashashi, Y.; Isobe, T.; Minoshima, S.; Fukuyama, R.; Shimizu, N.; Kuwano, R.
CS Res. Lab. Mol. Genet., Niigata Univ., Niigata, 951, Japan
SO Journal of Neuroscience Research (1992), 31(4), 600-5 CODEN: JNREDK; ISSN: 0360-4012
DT Journal
LA English
AB The nucleotide sequence is presented of a cDNA clone of mRNA encoding human 14-3-3 protein, a protein kinase-dependent activator of tyrosine and tryptophan hydroxylases and an endogenous inhibitor of protein kinase C. The 1730-nucleotide sequence of the cloned cDNA contains 191 bp of a 5'-noncoding region, the complete 738 bp of coding region, and 801 bp of a 3'-noncoding region contg. three canonical ***polyadenylation*** ***signals*** . The 14-3-3 protein .eta. chain cDNA encoded a polypeptide of 246 amino acids with a predicted mol. wt. 28,196. The predicted amino acid sequence of human 14-3-3 protein .eta. was highly homologous to that of previously reported bovine and rat 14-3-3 proteins with only two amino acid differences. The sequence carries structural features as putative regions responsible for activation of tyrosine and tryptophan hydroxylases and for inhibition of Ca2+/phospholipid-dependent protein kinase C. Northern blot anal. demonstrated widespread expression of the 14-3-3 protein .eta. chain in cultured cell lines derived from various human tumors. These ***findings*** suggest the conservative functions of the 14-3-3 protein among species. Spot blot hybridization anal. with flow-sorted chromosomes showed that the human 14-3-3 protein .eta. chain gene is assigned to chromosome 22.

L5 ANSWER 100 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:402318 CAPLUS
DN 119:2318
TI Characterization of the testes-specific pim-1 transcript in rat
AU Wingett, Denise; Reeves, Raymond; Magnuson, Nancy S.
CS Dep. Microbiol., Washington State Univ., Pullman, WA, 99164-4233, USA
SO Nucleic Acids Research (1992), 20(12), 3183-9 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB The pim-1 proto-oncogene encodes a serine/threonine protein kinase and is expressed in cells of hematolymphoid origin and in the germ cell lineages. In somatic cells, the pim-1 gene is expressed as a 2.8 kb transcript while a shorter sized transcript (2.3 kb) is expressed in rat testes. The shorter testes-specific pim-1 transcript was shown to arise through the use of an alternate ***polyadenylation*** ***signal*** present in the 3' untranslated region of the gene. This alternate polyadenylation event results in the removal of an A/U-rich regulatory element located in the 3' untranslated region of the pim-1 gene. This A/U-rich motif has been shown by a no. of labs. to destabilize the transcripts of genes that contain this sequence. Consistent with these ***findings*** , it was demonstrated that the shortened testes-specific pim-1 transcript is more stable than the longer A/U-rich contg. somatic transcript. Thus, the functional significance of different sized pim-1 transcripts may be directly related to their different stabilities and the greater stability of the testes-specific transcript may be essential for the translational delay obsd. in postmeiotic male germ cells.

L5 ANSWER 101 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:401113 CAPLUS
DN 119:1113
TI Genomic organization and expression of the human .alpha.1B-adrenergic receptor
AU Ramarao, Chodavarapu S.; Denker, Julie M. Kincade; Perez, Dianne M.; Gaivin, Robert J.; Riek, R. Peter; Graham, Robert M.
CS Res. Inst., Cleveland Clin. Found., Cleveland, OH, 44195, USA
SO Journal of Biological Chemistry (1992), 267(30), 21936-45 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB The cloning and the nucleotide sequence of the gene for the human .alpha.1B-adrenergic receptor (AR) are reported. It consists of 2 exons and a single large intron of at least 20 kilobases which interrupts the coding region at the end of the putative 6th transmembrane domain. The deduced amino acid sequence of the encoded receptor has a degree of homol. to the cloned hamster, rat, and dog .alpha.1B-ARs. To characterize the encoded protein, a fusion gene constructed by splicing together exon 1 and exon 2 was expressed transiently in COS-1 cell. The transfected gene fusion product resulted in the prodn. of an .alpha.1B-AR with ligand binding characteristics indistinguishable from those of the expressed hamster .alpha.1B cDNA. Evidence that the human .alpha.1B-AR gene is indeed transcribed is the ***finding*** of similar sized (2.8-kilobase) transcripts in human heart and other tissues by Northern blot anal. when either exon 1 or 2 is used as a probe. Moreover, using primers designed to span the exon 1/exon 2 boundary, a polymerase chain reaction product generated from single-stranded DNA prepd. from human heart mRNA had the exact size and nucleotide sequence predicted for a transcript in which exon 1 is spliced to exon 2. The 5'-flanking region (924 base pairs (bp)) of exon 1 contains neither a TATA box nor a CAAT box but is high in GC content (70%) and contains several Sp1 binding sites (GC boxes), consistent with promoters described for housekeeping genes. The 5'-untranslated region also contains a putative cAMP response element. Primer extension studies and RNase protection assays suggested that there are several potential transcription start sites in most tissues with a predominant site located 173 bp upstream from the translation start site. The 3'-flanking region contains a

putative ***polyadenylation*** ***signal*** (ATTAAA) 492 bp downstream from the stop codon. The genomic organization of the human .alpha.1B-AB with a single large intron interrupting its coding region differs from those of other ARs as well as muscarinic and 5-hydroxy-tryptamine receptors, which are intronless. The location of the intron in the human .alpha.1b-AR gene is also unique among those members of the G-protein-coupled receptor family that do possess introns. Availability of this gene will now allow further studies on the transcriptional control of human .alpha.1B-AR expression.

L5 ANSWER 102 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:251943 CAPLUS
DN 118:251943
TI In vivo generation of an adenylylcyclase isoform with a half-molecule motif
AU Katsushika, Shuichi; Kawabe, Junichi; Homcy, Charles J.; Ishikawa, Yoshihiro
CS Coll. Phys. Surg., Columbia Univ., New York, NY, 10032, USA
SO Journal of Biological Chemistry (1993), 268(4), 2273-6 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB A truncated form of adenylyl cyclase (type V-.alpha.) was cloned from a cardiac cDNA library. It constitutes a half-mol. of type V adenylyl cyclase diverging at the end of the 1st cytoplasmic loop. Northern blotting revealed the presence of such an mRNA species (.apprx.3.5 kilobases in size) in the heart. Genomic sequence anal. revealed that type V-.alpha. is generated via usage of a ***polyadenylation*** ***signal*** located within an intronic sequence of type V adenylyl cyclase gene. When type V-.alpha. is co-expressed with an artificially generated half-mol. constituting the latter half of type V adenylyl cyclase, the catalytic activity in transfected cell membranes is higher than that of controls. However, when either alone is overexpressed, no increase in catalytic activity results. These results indicate that a half-mol. of adenylyl cyclase, i.e. a protein contg. 6-transmembrane spans followed by a single cytoplasmic domain, can be generated in vivo, but catalytic activity is lacking unless heterodimerization can occur. This ***finding*** identifies another potential mechanism for generating diversity within this enzyme family.

L5 ANSWER 103 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:248995 CAPLUS
DN 118:248995
TI DNA sequence and transcriptional analyses of the region of the equine herpesvirus type 1 Kentucky A strain genome encoding glycoprotein C
AU Matsumura, Tomio; Smith, Richard H.; O'Callaghan, Dennis J.
CS Med. Cent., Louisiana State Univ., Shreveport, LA, 71130, USA
SO Virology (1993), 193(2), 910-23 CODEN: VIRLAX; ISSN: 0042-6822
DT Journal
LA English
AB DNA sequence and transcriptional analyses were performed on the region of the equine herpesvirus type 1 (EHV-1) genome (KyA strain) (map units 0.129 to 0.152) encoding open reading frames (ORFs) 15 and 16. ORF16 encodes a homolog of glycoprotein C of HSV-1 (herpes simplex virus type 1), while ORF15 corresponds in position to HSV-1 UL45 but exhibits no significant homol. at the amino acid level. Sequence analyses revealed that the EHV-1 gC ORF of 468 amino acids and ORF15 of 227 amino acids mapped at nucleotides (nt) 716 to 2119 and 2397 to 3077, resp. (relative to the 5' end of the BamHI recognition site at map unit 0.152). ORF15 exhibited significant homol. (69% identity) at the amino acid level to the EHV-4 gene located 3' of the EHV-4 gC homolog. Sequence analyses identified potential CAAT and TATA boxes for the EHV-1 gC ORF and a TATA box for ORF15. While no consensus ***polyadenylation*** ***signal*** was detected between ORFs 15 and 16, two ***polyadenylation*** ***signals*** were detected 3' of ORF15. Northern blot and S1 nuclease analyses were used to map and characterize the gC and ORF15 mRNAs, and metabolic inhibitors were used to identify the kinetic class of these two genes. The results revealed that gC is a .gamma.-1 gene which encodes a 2.8-kb mRNA, while ORF15 is a .gamma.-2 gene encoding a 0.9-kb mRNA which is 3' coterminal with the gC transcript. The gC and ORF15 mRNAs were shown by S1 nuclease analyses to initiate approx. 34 and 26 nucleotides downstream of their resp. TATA boxes and to have a common termination site 18 to 20 nucleotides downstream of a consensus ***polyadenylation*** ***signal*** . Comparative sequence anal. revealed that the KyA strain gC protein differs in only three amino acid residues from the gC protein of the EHV-1 Ab4 and T431 strains, and one of the three amino acid differences occurred within a segment of six contiguous amino acids showing a high degree of hydrophilicity in the gC mol. Further comparative sequence anal. revealed that the KyA strain genome has a major deletion in the region of ORF17 which lies 5' of gC in the Ab4 strain. This ***finding*** that 1038 base pairs (bp) of the 1203-bp ORF17 is deleted indicates that ORF17 is nonessential for EHV-1 replication in cell culture. To examine the regulation of the EHV-1 gC gene, transient transfection assays using CAT (chloramphenicol acetyltransferase) reporter gene constructs of gC were performed. The results showed that expression from the EHV-1 gC promoter required the presence of both the EHV-1 IE protein and the EHV-1 UL3 protein (an ICP27 homolog) for significant activation as has been shown with other EHV-1 late gene promoters.

L5 ANSWER 104 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:248781 CAPLUS
DN 118:248781
TI The right end of the unique region of the genome of human herpesvirus 6 U1102 contains a candidate immediate early gene enhancer and a homolog of the human cytomegalovirus US22 gene family
AU Thomson, B. J.; Honess, R. W.
CS Div. Virol., Natl. Inst. Med. Res., London, NW7 1AA, UK
SO Journal of General Virology (1992), 73(7), 1649-60 CODEN: JGVIAY; ISSN: 0022-1317
DT Journal
LA English
AB The nucleotide sequence of a 12 kbp HindIII fragment (HindIII C) from the right end of the unique component of the genome of human herpesvirus 6 (HHV-6) (strain U1102) was detd. The sequence has a mean G+C content of 42% and contains .apprx.28 copies of a tandemly repeated 104 to 107 bp element, which, with a single exception, contain a cleavage site for KpnI (the KpnI repeats). Each of these elements contains potential binding sites for transcription factors NF-.kappa.B and AP2. The KpnI repeats lie immediately upstream of a region previously identified as a candidate immediate early (IE) gene locus and therefore may constitute an IE gene enhancer element. One incomplete and 6 complete open reading frames (ORFs) were identified in the unique sequence of the HindIII C fragment. The predicted products of these ORFs do not include homologs of proteins encoded by members of the alpha- or gammaherpesvirus subfamily. However, the HindIII C fragment does contain a homolog of the US22 gene family, previously found only in the betaherpesvirus human cytomegalovirus (HCMV). These ***findings*** provide evidence that the close phylogenetic relationship between HHV-6 and HCMV is not

confined to the betaherpesvirus-specific arrangement of conserved replicative and structural genes which has been demonstrated previously.

L5 ANSWER 105 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:228514 CAPLUS
DN 118:228514
TI Molecular characterization/physiological properties of a new bioactive bovine seminal fluid protein (aSFP)
AU Einspanier, R.; Wempe, F.; Einspanier, A.; Scheit, K. H.; Schams, D.; Karg, H.
CS Tech. Univ. Muenchen, Freising, 8050, Germany
SO Molecular Andrology (1992), 4(3-4), 325-32 CODEN: MOANE3
DT Journal
LA English
AB An acidic protein (aSFP) has been isolated from bovine seminal fluid showing remarkable physiol. activities comparable to growth factors. Highly purified aSFP was characterized by 2-dimensional electrophoresis as a protein of 14 kDa with 2 different pI of 4.7 and 4.8. The bovine seminal vesicles/ampulla are the main source of aSFP. Immunoblot anal. was done to ***search*** for homologous proteins in other species. Detectable levels were present in bovine seminal plasma, but not in goat, sheep, pig and human. Concns. of aSFP in bovine seminal plasma were 1-6 mg/mL, detd. by an aSFP-specific RIA. Mitogenic activity of aSFP was demonstrated on bovine lymphocytes. There was an increase of cell no./progesterone release in bovine/rat uterus and ovarian granulosa cell cultures treated with aSFP (2-100 ng/mL). A cDNA expression library from bovine seminal vesicle tissue was screened by means of monospecific rabbit anti-aSFP IgGs. Clone pTF21 was sequenced; it contained an insert of 668 bp, with an open reading frame from position 7 to 411, from which a protein of 134 amino acids could be deduced. The mature aSFP was preceded by a signal peptide of 20 amino acids length. The protein sequence contained no signal for N-glycosylation. The start codon ATG is part of the sequence AAGATGA which fulfills the criteria of an initiation consensus sequence. The coding region was followed by 258 bp of the 3' untranslated region contg. the putative ***polyadenylation*** ***signal*** AATAAT. By Northern anal., aSFP mRNA is expressed in the seminal vesicle, in ampulla and weakly in epididymal tissue, but not in testis or other bovine tissues. ASFP is specified by a single-copy gene. Homologies to known protein sequences in a data base were not detected. Thus, aSFP is a member of a new protein family.

L5 ANSWER 106 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:207779 CAPLUS
DN 118:207779
TI Human cleavage signal-1 protein; cDNA cloning, transcription and immunological analysis
AU Javed, Ali A.; Naz, Rajesh K.
CS Dep. Obstet. Gynecol., Albert Einstein Coll. Med., Bronx, NY, 10461, USA
SO Gene (1992), 112(2), 205-11 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB The cleavage signal-1 protein (CS-1), a doublet antigen comprised of approx. 14-kDa and 18-kDa proteins is present on the surface of sperm of various mammalian species including humans. Polyclonal antibodies to CS-1 inhibit the early cleavage of fertilized eggs without apparently affecting sperm penetration and pronuclear formation. Here the cloning of the human CS-1 cDNA and its expression in vitro to obtain the recombinant protein (reCS-1) is reported. The CS-1 cDNA clone was isolated by immunol. screening of a human testis .lambda.gt11 cDNA library with monospecific polyclonal antibody against CS-1. The cDNA is 1828 bp long; from the start codon assigned to the first ATG (bp 98-100) it encodes a protein with 249 amino acid residues, terminating at TAA (bp 845-847). The cDNA isolated has a 97-bp 5'- and a 984-bp 3'-untranslated region. The potential ***polyadenylation*** ***signal*** (5'-AATAAA) is at bp 1803-1808. An extensive computer ***search*** of the GenBank database did not indicate extensive homol. with any known sequence, indicating that CS-1 is a unique protein. The CS-1 cDNA was cloned in the transcription vector pGEM-11Zf to obtain high-level in vitro transcription by SP6 and T7 RNA polymerase. The transcribed CS-1 RNA was translated in a rabbit reticulocyte in vitro translation system and produced a 33-kDa reCS-1 protein, as assessed by migration in a SDS-polyacrylamide gel. The polyclonal antibody against CS-1 specifically recognized the 33-kDa reCS-1 protein on Western blots of in vitro translated proteins, suggesting the authenticity of the cDNA clone.

L5 ANSWER 107 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:166650 CAPLUS
DN 118:166650
TI Cloning and characterization of cDNA encoding canine .alpha.-L- iduronidase. mRNA deficiency in mucopolysaccharidosis I dog
AU Stoltzfus, Lori J.; Sosa-Pineda, Beatriz; Moskowitz, Samuel M.; Menon, Kaushiki P.; Dlott, Bonnie; Hooper, Lucilla; Teplow, David B.; Shull, Robert M.; Neufeld, Elizabeth F.
CS Sch. Med., Univ. California, Los Angeles, CA, 90024, USA
SO Journal of Biological Chemistry (1992), 267(10), 6570-5 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB .alpha.-L-Iduronidase is a lysosomal enzyme, the deficiency of which causes mucopolysaccharidosis I (MPS I); a canine MPS I colony has been bred to test therapeutic intervention. The enzyme was purified to apparent homogeneity from canine testis and found to consist of two electrophoretically separable proteins that had common internal peptides but differed at their amino termini. A 57-base oligonucleotide, corresponding to the most probable codons of the longest peptide, was used to screen a canine testis cDNA library. Three cDNAs were isolated, two of which lacked the 5'-end whereas the third was full-length except for a small internal deletion. The composite sequence encodes an open reading frame of 655 amino acids that includes all sequenced peptides. The amino terminus of the larger protein, glutamic acid 26, is at the predicted signal peptide cleavage site, whereas the amino terminus of the smaller protein is leucine 106. There are six potential N-glycosylation sites and a noncanonical ***polyadenylation*** ***signal*** , CTTAAA. A ***search*** of GenBank showed that the amino acid sequence of .alpha.-L-iduronidase has similarity to that of a bacterial .beta.-xylosidase. A full-length cDNA corresponding to the composite sequence was constructed (pcIdu) and inserted into the pSVL expression vector (pSVcIdu). Two days after Cos-1 cells were transfected with pSVcIdu, their intracellular and secreted level of .alpha.-L-iduronidase activity had increased 8- and 22-fold, resp., over the endogenous activity. Fibroblasts of MPS I dogs, which have no .alpha.-L-iduronidase activity, lacked the normal .alpha.-L-iduronidase mRNA of 2.2 kilobases and contained instead a trace amt. of a 2.8-kilobase species. Isolation and characterization of an expressible .alpha.-L-iduronidase cDNA represents the first step toward mutation anal. and replacement therapy.

L5 ANSWER 108 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:162032 CAPLUS
DN 118:162032
TI Normal Chlamydomonas nuclear gene structure on linkage group XIX

AU Schloss, Jeffery A.; Croom, Henrietta Brown
CS Sch. Biol. Sci., Univ. Kentucky, Lexington, KY, 40506-0225, USA
SO Journal of Cell Science (1991), 100(4), 877-81 CODEN: JNCSAI; ISSN: 0021-9533
DT Journal
LA English
AB The unusual Chlamydomonas linkage group XIX, called the uni linkage group for the uni mutants that lack one of the paired flagellae of wild-type cells-has been reported to be phys. located exclusively at the basal bodies. To learn whether the structure of genes on this linkage group differs from the structure of nuclear genes in this organism, the primary structure of a gene that maps to linkage group XIX was detd. This anal. reveals the presence of 9 intervening sequences; the nucleotides at exon intron boundaries conform with nuclear gene intron junction sequences. Also typical for C. reinhardtii nuclear genes are the position and sequence of the putative ***polyadenylation*** ***signal*** . These ***findings*** suggest that transcripts from linkage group XIX are likely to be processed in the nucleus. The open reading frame, which displays weak but easily detected Chlamydomonas codon bias, potentially encodes a protein similar to a membrane anchor for cytoskeletal proteins. The observation that expression of this gene is regulated during interphase and in gametes is not consistent with the hypothesis that linkage group XIX may be expressed only during mitotic and meiotic processes.

L5 ANSWER 109 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:119145 CAPLUS
DN 118:119145
TI Isolation of the cDNA for erythrocyte integral membrane protein of 28 kilodaltons: member of an ancient channel family
AU Preston, Gregory M.; Agre, Peter
CS Sch. Med., Johns Hopkins Univ., Baltimore, MD, 21205, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1991), 88(24), 11110-14 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB CHIP28 is a 28-kDa integral membrane protein with similarities to membrane channels and is found in erythrocytes and renal tubules. A cDNA for CHIP28 was isolated from human fetal liver cDNA template by a three-step polymerase chain reaction (PCR) cloning strategy, starting with degenerate oligonucleotide primers corresponding to the N-terminal amino acid sequence detd. from purified CHIP28 protein. Using the third-step PCR product as a probe, a recombinant was isolated from a human bone marrow cDNA library. The combined sequence of the PCR products and bone marrow cDNA contains 38 base pairs of 5'-untranslated nucleotide sequence, an 807-bp open reading frame, and .apprxeq.2 kilobases of 3' untranslated sequence contg. a ***polyadenylation*** ***signal*** . This corresponds to the 3.1-kilobase transcript identified by RNA blot-hybridization anal. Authenticity of the deduced amino acid sequence of the CHIP28 protein C terminus was confirmed by expression and immunoblotting. Anal. of the deduced amino acid sequence suggests that CHIP28 protein contains six bilayer-spanning domains, two exofacial potential N-glycosylation sites, and intracellular N and C termini. ***Search*** of the DNA sequence data base revealed a strong homol. with the major intrinsic protein of bovine lens, which is the prototype of an ancient but recently recognized family of membrane channels. These proteins are believed for form channels permeable to water and possibly other small mols. CHIP28 shares homol. with all known members of this channel family, and it is speculated that CHIP28 has a similar function.

L5 ANSWER 110 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:2903 CAPLUS
DN 118:2903
TI Nucleotide and deduced amino acid sequences of the oxidosqualene cyclase from Candida albicans
AU Buntel, Christopher J.; Griffin, John H.
CS Dep. Chem., Stanford Univ., Stanford, CA, 94305-5080, USA
SO Journal of the American Chemical Society (1992), 114(24), 9711-13 CODEN: JACSAT; ISSN: 0002-7863
DT Journal
LA English
AB The DNA and predicted amino acid sequence of the oxidosqualene-lanosterol cyclase from the fungus Candida albicans is reported. This work was undertaken as the initial step in a program of reached directed at elucidating in detail the structural and functional basis for enzymic catalysis of polyene cyclization reactions. Portions of C. albicans genomic DNA sequences found by R. Kelly et al. (1990) to complement cyclase-deficient Saccharomyces cerevisiae mutants were subcloned and sequenced using the Sanger dideoxy chain-termination technol. This revealed an open reading frame of 2187 nucleotides (including stop codon) which is predicted to encode a 728 amino acid, 83.7 kDa protein. Consensus TATA box promoter and ***polyadenylation*** ***signal*** sequences were obsd. before the initiation codon and after the stop codon, resp. A ***search*** of the GenBank 71 and EMBL DNA sequence databases revealed no significant homologies to known gene sequences. A ***search*** of the PIR 31 and SWISS-PROT 21 protein sequence databases revealed a limited similarity to the human cholesteryl ester transferase. Direct comparison with the predicted amino acid sequence of the squalene-hopene cyclase from Bacillus acidocaldarius recently reported by D. Ochs et al. (1992) reveals four regions of substantial similarity, ranging from 29% identity over 77 residues to 46% identity over 37 residues. The C. albicans cyclase is predicted to have two notably hydrophobic regions which may be involved in the expected membrane localization by this enzyme. Both the C. albicans and B. acidocaldarius cyclases have regions of primary sequence rich in tryptophan and/or tyrosine residues. The electron-rich arom. sidechains of some of these residues may serve to stabilize cationic transition states and/or high-energy intermediates along the cyclization/rearrangement pathway.

L5 ANSWER 111 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1992:649594 CAPLUS
DN 117:249594
TI Expression of wild-type and mutant medium-chain acyl-CoA dehydrogenase (MCAD) cDNA in eukaryotic cells
AU Jensen, Thomas G.; Andresen, Brage S.; Bross, Peter; Jensen, Uffe Birk; Holme, Elisabeth; Koelvraa, Steen; Gregersen, Niels; Bolund, Lars
CS Inst. Hum. Genet., Univ. Aarhus, Aarhus, DK-8000, Den.
SO Biochimica et Biophysica Acta (1992), 1180(1), 65-72 CODEN: BBACAQ; ISSN: 0006-3002
DT Journal
LA English
AB An effective EBV-based expression system for eukaryotic cells has been developed and used for the study of the mitochondrial enzyme medium-chain acyl-CoA dehydrogenase (MCAD). 1325 Bp of PCR-generated MCAD cDNA, contg. the entire coding region, was placed between the SV40 early promotor and ***polyadenylation*** ***signals*** in the EBV-based vector. Both wild-type MCAD cDNA and cDNA contg. the prevalent disease-causing mutation A to G at position 985 of the MCAD cDNA were tested. In transfected COS-7 cells, the steady state amt. of mutant MCAD protein was consistently lower than the amt. of wild-type human enzyme. The enzyme activity in exts.

from cells harboring the wild-type MCAD cDNA was dramatically higher than in the controls (harboring the vector without the MCAD gene) while only a slightly higher activity was measured with the mutant MCAD. The mutant MCAD present behaves like wild-type MCAD with respect to soly., subcellular location, mature protein size and tetrameric structure. In immunoblot comparisons, the MCAD protein was present in normal fibroblasts, but essentially undetectable in patient fibroblasts homozygous for the prevalent mutation. The authors suggest that the MCAD protein carrying this mutation has an impaired ability to form correct tetramers, leading to instability and subsequent degrdn. of the enzyme. This ***finding*** is discussed in relation to the results from expression of human MCAD in Escherichia coli, where preliminary results show that prodn. of mutant MCAD leads to the formation of aggregates.

L5 ANSWER 112 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1992:627380 CAPLUS
DN 117:227380
TI Cloning and expression of a new human polypeptide which regulates protein phosphorylation in Escherichia coli
AU Daniele, Aurora; Altruda, Fiorella; Ferrone, Merina; Silengo, Lorenzo; Chiarantini, Laura; Bianchi, Marzia; Stocchi, Vilberto; Magnani, Mauro
CS Dip. Genet. Biol. Chim. Med., Univ. Torino, Turin, Italy
SO Molecular and Cellular Biochemistry (1991), 107(2), 87-94 CODEN: MCBIB8; ISSN: 0300-8177
DT Journal
LA English
AB A 1820 bp full-length clone encoding for a new human protein was isolated from a .lambda.gt11 placental cDNA library using anti-human hexokinase antibodies. The cDNA complete sequence includes a 12 bp 5'noncoding region, a single open reading frame encoding a protein of 55 KDa (HP-10) and a 177 bp non-coding region with two putative ***polyadenylation*** ***signals*** upstream of the 3' poly(A) tail. The deduced amino acid sequence reveals a sequence of 492 amino acids that contains a stretch of 7 glutamic acids from position 169 and one potential glycosylation site at position 274. Although antibodies against hexokinase recognize the fusion protein and antibodies against the fusion protein recognize hexokinase, HP-10 is not human hexokinase, by a no. of criteria including the alignment of detd. amino acid sequences. In ***searching*** for a possible functional role of HP-10 its cDNA was inserted into a prokaryotic vector which allows the expression of the non-fused protein. Bacteria expressing the HP-10 encoded protein were isolated and found to have a dramatic increase in endogenous phosphorylated proteins. Since HP-10 does not have a protein kinase activity per se it should be considered a new regulatory phosphorylation protein which is active in E. coli.

L5 ANSWER 113 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1992:487355 CAPLUS
DN 117:87355
TI Origin of the two mRNA species for the human neurofilament light gene
AU Beaudet, Lucille; Charron, Guy; Julien, Jean Pierre
CS Cent. Res. Neurosci., McGill Univ., Montreal, QC, H3G 1A4, Can.
SO Biochemistry and Cell Biology (1992), 70(5), 279-84 CODEN: BCBIEQ; ISSN: 0829-8211
DT Journal
LA English
AB The human neurofilament light (hNF-L) gene yields 2 major species of mRNAs of 2.4 and 3.8 kilobases (kb) in size. To investigate the origin of these 2 mRNAs, the expression of hNF-L DNA fragments including different lengths 5'-flanking regions were analyzed in transgenic mice. The ***finding*** that the 3.8-kb mRNA species is produced by an nHF-L transgene that includes only the proximal promoter region (-0.3 kb) demonstrates that both the 2.4- and 3.8-kb mRNAs are derived from the same site of transcription initiation. Sequencing of the 3'-untranslated region of the nNF-L gene revealed the presence of multiple AATAAA ***polyadenylation*** ***signals*** . It is concluded from Northern blotting expts. using probes spanning various regions of the hNF-L gene that the 2.4- and 3.8-kb mRNAs originate from the selective use of ***polyadenylation*** ***signals*** located 1.4 kb apart.

L5 ANSWER 114 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1992:1477 CAPLUS
DN 116:1477
TI The genomic organization of the CD28 gene. Implications for the regulation of CD28 mRNA expression and heterogeneity
AU Lee, Kelvin P.; Taylor, Carol; Petryniak, Bronislawa; Turka, Laurence A.; June, Carl H.; Thompson, Craig B.
CS Med. Cent., Univ. Michigan, Ann Arbor, MI, 48109, USA
SO Journal of Immunology (1990), 145(1), 344-52 CODEN: JOIMA3; ISSN: 0022-1767
DT Journal
LA English
AB CD28 is a 90-kDa homodimeric glycoprotein present on the surface of a large subset of T cells that appears to play an important role in the modulation of T cell activation. Although a no. of physiol. effects assocd. with CD28 stimulation have been defined, relatively less is known about the structure and expression of the CD28 gene itself. CD28 is expressed in both Th cells and plasma cells as a series of four distinct CD28 mRNA species: 1.3-, 1.5-, 3.5-, and 3.7-kb transcripts. The steady state expression of all four transcripts in CD28+ T cells was stimulated by PMA, suggesting that they might share a common phorbol-sensitive promoter. Consistent with this hypothesis, CD28 was found to be encoded by a single copy gene organized into four exons, each exon defining a functional domain of the predicted protein. All CD28 transcripts appear to initiate within a 61-bp palindrome. Generation of the four CD28 mRNA species from the CD28 gene involves two distinct posttranscriptional events. The longer pair of transcripts (3.5/3.7 kb) is generated by the use of an alternate nonconsensus ***polyadenylation*** ***signal*** . This results in the addn. of 2167 bp beyond the first polyadenylation site utilized by the shorter (1.3/1.5 kb) pair of transcripts. The size difference between the 3.7- and 3.5-kb messages and between the 1.5- and 1.3-kb messages is generated by an internal splicing event that deletes 252 bp within exon 2, which encodes the extracellular domain. This deletion would result in the loss of 84 amino acids, including 4 of 5 extracellular cysteine residues. Although this deletion would result in significant disruption of CD28 secondary structure, it would not be expected to interfere with the ability of the resultant protein to be expressed on the cell surface. These ***findings*** suggest that variant iso-types of CD28 may be expressed on the cell surface with potentially different physiol. roles.

L5 ANSWER 115 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1991:625212 CAPLUS
DN 115:225212
TI Isolation of a cathepsin B-encoding cDNA from murine osteogenic cells
AU Friemert, Constanze; Closs, Ellen I.; Silbermann, Michael; Erfle, Volker; Strauss, P. Guenter
CS Abt. Mol. Zellpathol., GSF-Forschungszent. Umwelt und Gesundheit G.m.b.H., Neuherberg, D(W)-8042, Germany

SO Gene (1991), 103(2), 259-61 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB Cathepsin B-encoding cDNA (CTSB) clones have been isolated from a .lambda.gt10 library of a murine osteosarcoma by differential screening during a ***search*** for genes which are typically expressed during osteogenic differentiation in mouse mandibular condyles in vitro. Sequencing of the CTSB 3' end revealed that the isolated sequence contained an 825-bp 3'-noncoding region, the ***polyadenylation*** ***signal*** and the poly(A) tail. The enhanced CTSB expression during the early stages of the enchondral ossification-like process in mandibular codyles in vitro suggests that CTSB participates in the degrdn. of cartilage matrix prior to the synthesis of bone matrix proteins.

L5 ANSWER 116 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1991:241552 CAPLUS
DN 114:241552
TI Lymphoproliferative disease virus of turkeys: sequence analysis and transcriptional activity of the long terminal repeat
AU Gak, Eva; Yaniv, Abraham; Sherman, Levana; Ianconescu, Marius; Tronick, Steven R.; Gazit, Arnona
CS Sackler Sch. Med., Tel-Aviv Univ., Tel-Aviv, 69978, Israel
SO Gene (1991), 99(2), 157-62 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB The lymphoproliferative disease virus (LPDV) is the etiol. agent of a lymphoproliferative disease that naturally occurs in turkeys. Recently, the LPDV provirus was cloned and established as a replication-competent genome devoid of a viral oncogene (Gak, E., et al., 1989). This report presents the nucleotide sequence of its long terminal repeat (LTR) and establishes it as a potent transcriptional element. Several features of the LPDV LTR were similar to those found in the LTRs of the avian sarcoma-leukemia viruses (ASLV) and include the primer-binding site (tRNATrp), the polypurine tract, the organization of the ***polyadenylation*** ***signal*** , the complexities of the U3, R and U5 regions, as well as a potential secondary structure in U5-R. The LTR sequence diverges significantly from the ASLV LTRs, which share a common structure and have extensive sequence homol. mainly in the R and U5 domains. These ***findings*** support the conclusion that LPDV represents a distinct class of avian retrovirus, evolutionarily related to the ASLV family.

L5 ANSWER 117 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1991:158150 CAPLUS
DN 114:158150
TI Nucleotide sequence of a radish cDNA clone coding for a late embryogenesis abundant (LEA) protein
AU Raynal, M.; Gaubier, P.; Grellet, F.; Delseny, M.
CS Lab. Physiol. Veg., CNRS, Perpignan, 66025, Fr.
SO Nucleic Acids Research (1990), 18(20), 6132 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB The sequence of a cDNA clone, RSLEA2, corresponding to a radish dry seed abundant mRNA is reported. It was selected from a dry seed cDNA library screened successively with single-stranded cDNA probes prepd. from immature seeds (30 DAF), dry seeds and 24 h-old seedling poly(A) RNA. RSLEA2 showed a strong hybridization signal only with the homologous probe. The nucleotide sequence was detd. by the Sanger method using T7 DNA polymerase on alkali-denatured supercoiled plasmids. The cDNA is 744 bp in length and hybridizes to a unique class of mRNAs of approx. the same size (not shown). Only one plausible ORF was identified, and the initiation site was detd. by comparison with consensus sequences. The deduced protein is very hydrophilic, as are most other Lea proteins and consists of 184 aa residues corresponding to a mol. wt. of 19 kDa. A potential ***polyadenylation*** ***signal*** AATAAA is found in the 3'-noncoding region, 155 nt upstream from the poly(A) tail. A ***search*** for polypeptide homologies in data banks has revealed strong local similarities with a particular family of plant seed proteins (Lea D11 in cotton, RAB21 in rice, RAB17 in maize or dehydrin in barley. These genes have been shown to respond to ABA and also to water stress in leaves. Particularly remarkable is a stretch of 8 serine residues which is conserved in all these proteins.

L5 ANSWER 118 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1991:158102 CAPLUS
DN 114:158102
TI Human .alpha.-N-acetylgalactosaminidase - molecular cloning, nucleotide sequence, and expression of a full-length cDNA. Homology with human .alpha.-galactosidase A suggests evolution from a common ancestral gene
AU Wang, Anne M.; Bishop, David F.; Desnick, Robert J.
CS Div. Med. Mol. Genet., Mount Sinai Sch. Med., New York, NY, 10029, USA
SO Journal of Biological Chemistry (1990), 265(35), 21859-66 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Human .alpha.-N-acetylgalactosaminidase (.alpha.-GalNAc), the lysosomal glycohydrolase that cleaves .alpha.-N-acetylgalactosaminyl moieties from glycoconjugates, is encoded by a gene localized to chromosome 22q13.fwdarw.qter. The deficient activity of .alpha.-GalNAc is the enzymic defect in Schindler disease, an inherited neuroaxonal dystrophy. To isolate a full-length cDNA, the enzyme from human lung was purified to homogeneity, 129 non-overlapping amino acids were detd. by microsequencing the NH2 terminus and seven tryptic peptides, and four synthetic oligonucleotide mixts. were used to screen a human fibroblast cDNA library. A full-length cDNA, pAGB-3, isolated from a placental .lambda.gt11 cDNA library, had a 2158-base-pair (bp) insert with an open reading frame which predicted an amino acid sequence that was colinear with all 129 microsequenced residues of the purified enzyme. The pAGB-3 insert had a 344-bp 5'-untranslated region, a 1236-bp open reading frame encoding 411 amino acids, a 514-bp 3'-untranslated region, and a 64-bp poly(A) tract. A signal peptide sequence of 17 amino acids as well as six N-glycosylation sites were predicted. The pAGB-3 cDNA was subcloned into the p91023(B) mammalian expression vector and human .alpha.-GalNAc activity was transiently expressed in COS-1 cells, demonstrating the functional integrity of the full-length cDNA. Northern hybridization anal. of mRNA revealed two transcripts of about 3.6 and 2.2 kilobases (kb), and primer extension studies indicated a cap site at nucleotide -347 for the 2.2 kb transcript. The 3.6-kb cDNA (pAGB-35) subsequently was isolated which resulted from alternative polyadenylation. The 3598-bp pAGB-35 insert was identical to that of the 2.2-kb insert but had addnl. 5'- and 3'-untranslated sequences including a second downstream ***polyadenylation*** ***signal*** at nucleotide 3100-3105. Isolation of a genomic clone, gAGB-1, and sequencing the 2048-bp region including pAGB-3 revealed a 1754-bp intron between codons 319 and 320, which also was the the site of a 70-bp insertion and a 45-bp deletion in other cDNA clones. Notably, the .alpha.-GalNAc cDNA had remarkable amino acid homol. with the human .alpha.-galactosidase A (.alpha.-Gal A) cDNA, suggesting the evolutionary relatedness of these genes. The .alpha.-GalNAc

cDNA had 46.9-64.7%% amino acid identity in sequences (codons 1-319) corresponding to .alpha.-Gal A exons 1 through 6, while the comparable exon 7 sequence (pAGB-3 codons 320-411) had only 15.8% homol. with numerous gaps. These ***findings*** implicate the genomic region at and surrounding codon 319 as a potential site for the abnormal processing of .alpha.-GalNAc transcripts as well as for a recombinational event in the evolution and divergence of .alpha.-Gal A and .alpha.-GalNAc. The availability of the full-length cDNA for human .alpha.-GalNAc will permit studies of the genomic organization and evolution of this lysosomal gene, as well as the characterization of the mol. lesions causing Schindler disease.

L5 ANSWER 119 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1991:157844 CAPLUS
DN 114:157844
TI The nucleotide sequence of abutilon mosaic virus reveals prokaryotic as well as eukaryotic features
AU Frischmuth, T.; Zimmat, G.; Jeske, H.
CS Inst. Allg. Bot., Hamburg, D-2000/52, Germany
SO Virology (1990), 178(2), 461-8 CODEN: VIRLAX; ISSN: 0042-6822
DT Journal
LA English
AB The complete nucleotide sequence of abutilon mosaic virus (West Indian isolate, AbMVa) is presented. The resulting genomic structure resembles that of other geminiviruses which are transmitted by the whitefly (Bemisia tabaci: AbMV possesses a bipartite circular genome with bidirectional orientation of the open reading frames (ORF). Both components have a common region of 180 bases with 99% homol. while the rest of their sequence is distinct. Eukaryotic regulatory transcription elements precede most ORFs and ***polyadenylation*** ***signals*** are present at the end of most ORFs. However, 2 ORFs show features of prokaryotic genes. This chimeric genome organization is discussed with ref. to the ***finding*** that AbMV DNA is present in plastids as well as in the nucleus of infected cells.

L5 ANSWER 120 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1991:18508 CAPLUS
DN 114:18508
TI Nucleotide and deduced amino acid sequence of an aspartic proteinase inhibitor homolog from potato tubers (Solanum tuberosum L.)
AU Strukelj, B.; Pungercar, J.; Ritonja, A.; Krizaj, I.; Gubensek, F.; Kregar, I.; Turk, V.
CS Dep. Biochem., Jozef Stefan Inst., Ljubljana, 61111, Yugoslavia
SO Nucleic Acids Research (1990), 18(15), 4605 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB Two protein inhibitors of aspartic proteinases were isolated from potato tubers and sequenced. In order to ***find*** related inhibitors, several cDNA clones were isolated from a potato tuber lambda gt11 cDNA library encoding aspartic proteinase inhibitor homologs. The longest, full-length clone contains an open reading frame of 660 bp coding for a protein of 220 amino acid residues. The deduced protein sequence shows about 94% and 99% similarity to the novel inhibitor of cathepsin D and potato cathepsin D inhibitor, resp. The presumed signal peptide and 2 ***polyadenylation*** ***signals*** are underlined.

L5 ANSWER 121 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1990:527396 CAPLUS
DN 113:127396
TI Amino acid sequence of a novel integrin .beta.4 subunit and primary expression of the mRNA in epithelial cells
AU Suzuki, Shintaro; Naitoh, Yuji
CS Sch. Med., Univ. South. California, Los Angeles, CA, 90033, USA
SO EMBO Journal (1990), 9(3), 757-63 CODEN: EMJODG; ISSN: 0261-4189
DT Journal
LA English
AB The polymerase chain reaction was used to isolate cDNA clones that encode a new integrin .beta. subunit-.beta.4. Its cDNA, which is 5676 bp in length, has 1 long coding sequence (5256 bp), a ***polyadenylation*** ***signal*** , and a poly(A) tail. The deduced sequence of 1752 amino acids is unique among the integrin .beta. subunits. It contains a putative signal sequence as well as a transmembrane domain that divides the mol. into an extracellular domain at the N-terminal side and a cytoplasmic domain at the C-terminal side. The extracellular domain exhibits a 4-fold repeat of cysteine-rich motif similar to those of other integrin .beta. subunits. Certain features of the extracellular domain, however, are unique to the .beta.4 subunit sequence. Of the 56 conserved cysteine residues found within the extracellular domain of other mature .beta. subunits, 8 such residues are deleted from the .beta.4 subunit sequence. The cytoplasmic domain is much larger (.apprx.1000 amino acids) than those of other .beta. subunits (.apprx.50 amino acids) and has no significant homol. with them. A protein homol. ***search*** revealed that the .beta.4 subunit cytoplasmic domain has 4 repeating units that are homologous to the type III repetition exhibited by fibronectin. The .beta.4 subunit mRNA was expressed primarily in epithelial cells. The restricted expression and the new structural features distinguish the integrin .beta.4 subunit from other integrin .beta. subunits.

L5 ANSWER 122 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1990:492168 CAPLUS
DN 113:92168
TI Hepatitis delta virus genome replication: a polyadenylated mRNA for delta antigen
AU Hsieh, Sen Yung; Chao, Mei; Coates, Laura; Taylor, John
CS Fox Chase Cancer Cent., Philadelphia, PA, 19111, USA
SO Journal of Virology (1990), 64(7), 3192-8 CODEN: JOVIAM; ISSN: 0022-538X
DT Journal
LA English
AB Hepatitis delta virus (HDV) replicates its genome in the nucleus of an infected cell. However, an unsolved problem has been the identification in the cytoplasm of a putative mRNA for the synthesis of the only virus-coded protein, the delta antigen. This report describes the characterization of an 800-base RNA that is cytoplasmic, polyadenylated, and antigenomic and that should direct the translation of the delta antigen. This RNA was about 500 times less abundant than full-length genomic RNA. The predominant 5' terminus and the 3' site at which the poly(A) is added were mapped. At a point 15 to 20 bases upstream of the poly(A) addn. site is the sequence AAUAAA, which could have been used as a ***signal*** for the ***polyadenylation*** . When an infectious cDNA clone of the whole HDV genome was changed at this site to UUUAAA, the clone was no longer infectious and it was unable to direct the synthesis of the delta antigen. These ***findings*** provided addnl. evidence that the polyadenylated RNA was at least the predominant method for the expression of the delta antigen. Apparently, the HDV RNA was processed as if it were a host mRNA polymerase II transcript, although this did not necessarily indicate that HDV RNA was transcribed with this enzyme.

L5 ANSWER 123 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1990:453242 CAPLUS
DN 113:53242
TI Structure and transcription of the glycoprotein gene of attenuated HEP-Flury strain of rabies virus
AU Morimoto, Kinjiro; Ohkubo, Akemi; Kawai, Akihiko
CS Fac. Pharm. Sci., Kyoto Univ., Kyoto, 606, Japan
SO Virology (1989), 173(2), 465-77 CODEN: VIRLAX; ISSN: 0042-6822
DT Journal
LA English
AB The mRNA-encoding G protein of the attenuated HEP-Flury strain of rabies virus was sequenced by the cDNA cloning technique. The G mRNA was composed of 2059 nucleotides, with the coding region located from the 28th to 1602nd nucleotide, and was capable of encoding a polypeptide of k524 amino acids. Although the coding region was highly homologous (.gtoreq.90%) to that of ERA and PV strains, the 3'-noncoding region of the HEP virus G mRNA was longer than that reported for other strains by .apprx.400 nucleotides. The extra sequence was homologous to the long G-L intergenic sequence of the PV viral genome. The HEP virus genome lacked the postulated ***polyadenylating*** ***signal*** (TGAAAAAAAA) that should have been found just before the long G-L intergenic region, which indicates that the long G-L intergenic region of the HEP virus is integrated into the preceding G gene, and is transcribed only as a portion of the G-mRNA mol. In the ERA virus-infected cells, however, 2 species of G-mRNA (1.9 and 2.3 kb long) were produced. The longer G mRNA also contained the sequence complementary to the long G-L intergenic region, and the shorter one did not. These ***findings*** suggest that 2 different poly(A)-tailing signals (one is present just before and another at the end of the long G-L intergenic region) work toward terminating the transcription of the ERA virus G gene and that the longer G mRNA is produced as a readthrough product.

L5 ANSWER 124 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1990:401398 CAPLUS
DN 113:1398
TI Vertebrate protamine gene evolution I. Sequence alignments and gene structure
AU Oliva, Rafael; Dixon, Gordon H.
CS Fac. Med., Univ. Calgary, Calgary, AB, T2N 4N1, Can.
SO Journal of Molecular Evolution (1990), 30(4), 333-46 CODEN: JMEVAU; ISSN: 0022-2844
DT Journal
LA English
AB The availability of the amino acid sequence for 9 different mammalian P1 family protamines and the revised amino acid sequence of the chicken protamine galline reveals a much closer relation between mammalian and avian protamines than was previously thought. Dot matrix anal. of all protamine genes for which genomic DNA or cDNA sequence is available reveals both marked sequence similarities in the mammalian protamine gene family and internal repeated sequences in the chicken protamine gene. The detailed alignments of the cis-acting regulatory DNA sequences shows several consensus sequence patterns, particularly the conservation of a cAMP response element (CRE) in all the protamine genes and of the regions flanking the TATA box, CAP site, N-terminal coding region, and ***polyadenylation*** ***signal*** . In addn., there was a high frequency of the CA dinucleotide immediately adjacent to the CRE element of both the protamine genes and the testis transition proteins, a feature not present in other genes, which suggests the existence of an extended CRE motif involved in the coordinate expression of protamine and transition protein genes during spermatogenesis. Overall, these ***findings*** suggest the existence of an avian-mammalian P1 protamine gene line and are discussed in the context of different hypotheses for protamine gene evolution and regulation.

L5 ANSWER 125 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1990:173276 CAPLUS
DN 112:173276
TI A single gene codes for two forms of rat nucleolar protein B23 mRNA
AU Chang, Jin Hong; Olson, Mark O. J.
CS Med. Cent., Univ. Mississippi, Jackson, MS, 39216-4505, USA
SO Journal of Biological Chemistry (1989), 264(20), 11732-7 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Protein B23 (38 kDa, pI = 5.1) is an abundant RNA-assocd. nucleolar phosphoprotein and putative ribosome assembly factor. A full-length cDNA clone (.lambda.JH1) encoding a major expressed form of rat protein B23, now designated B23.1, has been reported. Here, the isolation from a rat brain library and sequence of a cDNA clone (.lambda.JH2) coding for a second form (B23.2) of protein Bi3 are reported. Isoforms B23.1 and B23.2 are polypeptides of 292 and 257 amino acids, resp. The 5'-untranslated regions of the 2 cDNAs and the N-terminal 255 amino acids of the proteins are identical in the 2 isoforms. However, the 3'-untranslated regions of the mRNAs are completely different, and the dipeptide Gly-Gly in B23.1 (residues 256 and 257) is replaced by Ala-His in B23.2, indicating that the former is not a precursor of the latter. The ***finding*** of AGGT sequences in the 3' regions of .lambda.JH1 suggest the presence of intron-exon boundaries at the point where the 2 cDNAs begin to differ. To investigate the origin of the 2 isoforms, 2 rat genomic libraries were screened with oligonucleotide probes based on sequences from the unique regions of the 2 cDNAs. One of the genomic clones isolated (.lambda.JH125) contained a 6.5-kilobase fragment encoding the 3' end of both cDNAs. .lambda.JH125 contains 4 exons designated W, X, Y, and Z in the order indicated. Exons W and X encode 36 amino acids at the carboxyl terminus of B23.2, whereas exons W, Y, and Z encode the carboxyl-terminal 71 amino acid residues of B23.1. Exons X and Z each contain distinct 3'-untranslated sequences in which are found ***polyadenylation*** ***signals*** . Evidently, 2 different mRNAs are formed by alternative splicing of sep. 3' segments onto a common 5' region.

L5 ANSWER 126 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1990:92832 CAPLUS
DN 112:92832
TI Cloning and nucleotide sequence of a full-length cDNA for human 14 kDa .beta.-galactoside-binding lectin
AU Hirabayashi, Jun; Ayaki, Hitoshi; Soma, Genichiro; Kasai, Kenichi
CS Fac. Pharm. Sci., Teikyo Univ., Sagamiko, 199-01, Japan
SO Biochimica et Biophysica Acta (1989), 1008(1), 85-91 CODEN: BBACAQ; ISSN: 0006-3002
DT Journal
LA English
AB A full-length cDNA for a 14K-type human lung .beta.-galactoside-binding lectin was cloned. The cDNA includes a 405 bp open reading frame coding 135 amino acids including the initiator methionine, and having a single internal EcoRI site and a ***polyadenylation*** ***signal*** . The deduced amino-acid sequence agreed completely with the sequence of a human placenta lectin detd. by direct amino-acid sequence anal. It showed extensive sequence similarity with other vertebrate 14K-type lectins and a 35K-type lectin (carbohydrate-binding protein 35) of mouse 3T3 cell. ***Search*** of a Genbank sequence

data base revealed significant sequence similarity between the .beta.-galactoside-binding lectins and the carboxyl-terminal half of an IgE-binding protein, the cDNA of which has been cloned from rat basophilic leukemia cells. Thus, 14K-type lectin, 35K-type lectin and IgE-binding protein appeared to form a superfamily of proteins. Almost all invariant residues are located in the central region of the 14K-type lectins, so this region may constitute an essential part of the lectins, such as the sugar-binding domain.

L5 ANSWER 127 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1990:71137 CAPLUS
DN 112:71137
TI Polyadenylation function and sequence variability of the long terminal repeats of the human endogenous retrovirus-like family RTVL-H
AU Mager, Dixie L.
CS B. C. Cancer Res. Cent., Univ. British Columbia, Vancouver, BC, V5Z 1L3, Can.
SO Virology (1989), 173(2), 591-9 CODEN: VIRLAX; ISSN: 0042-6822
DT Journal
LA English
AB The RTVL-H family of human endogenous retrovirus-like sequences consists of .apprx.1000 full-length elements and at least as many solitary RTVL-H related long terminal repeats (LTRs). Some cDNA clones from 2 human cell libraries (Hep-2 and normal peripheral blood) were characterized, and 3 clones in which the AATAAA signal within the RTVL-H LTR has functioned to polyadenylate the transcript were identified. In 2 of these cases, the LTR has provided the ***polyadenylation*** ***signal*** for non-RTVL-H initiated transcriptional units. The DNA sequences of the LTR regions from these 2 cDNA clones are significantly different from a consensus LTR sequence generated from 10 genomic LTRs. In fact, two of these cDNA-derived LTRs, although closely related to each other, have a subregion within them which is not found in the genomic LTRs that have been analyzed. LTRs contg. this subregion, termed type II LTRs, comprise .apprx.25% of the total genomic LTR population. In stable DNA transfection expts., both a type I and a type II LTR were able to donate a functional ***polyadenylation*** ***signal*** to a neomycin-resistance gene. In LTR-pos. placental cDNA clones, type II LTRs were found more frequently than expected from their genomic abundance. These ***findings*** suggests that RTVL-H LTRs may provide 3' processing signals for a variety of human RNAs. They also indicate that distinct subpopulation of RTVL-H LTRs can be distinguished and suggest that this or other subpopulations may have different functional capacities in different human cells.

L5 ANSWER 128 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1990:1781 CAPLUS
DN 112:1781
TI Efficient functioning of plant promoters and poly(A) sites in Xenopus oocytes
AU Ballas, Nurit; Broido, Shimshon; Soreq, Hermona; Loyter, Abraham
CS Life Sci. Inst., Hebrew Univ., Jerusalem, 91904, Israel
SO Nucleic Acids Research (1989), 17(19), 7891-903 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB Mature Xenopus oocytes were challenged with DNA constructs including plant regulatory elements, namely, the cauliflower mosaic virus (CaMV) 35S promoter as well as the plasmid nopaline synthase (NOS) promoter and ***polyadenylation*** ***signal*** . Bacterial chloroamphenicol acetyltransferase (CAT) was used as a reporter gene. When microinjected into these cells, the plant-derived DNA constructs effectively promoted CAT synthesis in a manner dependent on the presence of the plant promoters and probably also on the ***polyadenylation*** ***signals*** . Structural studies revealed that the supercoiled structures of the above DNA plasmids were much more active in supporting CAT synthesis in microinjected oocytes than their linear forms, with clear correlation between efficient gene expression and DNA topol. In contrast, the linear forms of these plasmids were considerably more active than the supercoiled ones in transfected plant protoplasts. These ***findings*** demonstrate, for the first time, the activity of regulatory elements from plant genes in Xenopus oocytes and shed new light on the specific rules applicable for gene expression in plant and animal cells.

L5 ANSWER 129 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1988:584814 CAPLUS
DN 109:184814
TI Multiple abnormal .beta.-hexosaminidase .alpha. chain mRNAs in a compound-heterozygous Ashkenazi Jewish patient with Tay-Sachs disease
AU Ohno, Kousaku; Suzuki, Kunihiko
CS Sch. Med., Univ. North Carolina, Chapel Hill, NC, 27599, USA
SO Journal of Biological Chemistry (1988), 263(34), 18563-7 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Abnormal .beta.-hexosaminidase .alpha. chain cDNA clones were isolated from fibroblasts of an Ashkenazi Jewish patient with Tay-Sachs disease. Four abnormal cDNA clones were sequenced in their entirety. Three of these mRNAs retained intron 12 with a mutation from G to C at the 5' donor site, and the patient was heterozygous with respect to this splicing defect. One clone retained, in addn. to intron 12, intron 13, which was truncated and polyadenylated due to a ***polyadenylation*** ***signal*** within intron 13. The 4th clone did not contain intron 12 and was missing exon 12. Some of these abnormal mRNAs were also missing 1 or more of the upstream exons. The regions of exon 12-intron 12 and of upstream exons were evaluated in a total of 30 clones, including those completely sequenced, by restriction mapping and Southern anal. with appropriate probes. Of the 25 cDNA clones that included the exon 12-intron 12 region, 11 contained the exon 12-intron 12 sequence with the junctional transversion, and 11 were missing both exon 12 and intron 12. Among the 12 clones that included the region of exon 3-exon 9, 7 were missing 1 or more of the upstream exons. Three clones gave results expected of normal cDNA in the region of exons 12 and 13. One of the 3, furthermore, was 3.6-kilobases long and contained the completely normal .beta.-hexosaminidase .alpha. chain mRNA sequence on the 3' side and an abnormal 1.7-kilobase segment at the 5' end. These ***findings*** suggest that the splicing defect results in either retention of intron 12 or skipping of exon 12 in approx. equal proportions and that remote upstream exons are also frequently excised out. The 3 clones that were normal in the exon 12-intron 12 region could have derived from the other yet-to-be-characterized mutant allele. However, firm evidence that the abnormal upstream sequence is directly related to Tay-Sachs disease was not obtained.

L5 ANSWER 130 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1988:523374 CAPLUS
DN 109:123374
TI A rabbit .beta.-globin ***polyadenylation*** ***signal*** directs efficient termination of transcription of polyomavirus DNA
AU Lanoix, Jacqueline; Acheson, Nicholas H.

CS Dep. Microbiol. Immunol., McGill Univ., Montreal, QC, H3A 2B4, Can.
SO EMBO Journal (1988), 7(8), 2515-22 CODEN: EMJODG; ISSN: 0261-4189
DT Journal
LA English
AB A viable insertion mutant (ins 5) of polyomavirus was constructed which contains, upstream of the L-strand ***polyadenylation*** ***signal*** , a 94-nt fragment of rabbit .beta.-globin DNA. Included in this fragment are all of the sequence elements required for efficient cleavage and polyadenylation of rabbit .beta.-globin RNA. The .beta.-globin signal was efficiently recognized by the cleavage/polyadenylation machinery in mouse 3T6 cells infected with ins 5, signaling >90% of the polyadenylation events on L-strand RNAs. Furthermore, the presence of this efficient ***polyadenylation*** ***signal*** resulted in a 1.4-2.5-fold increase in the fraction of virus-specific RNAs that were polyadenylated. Most importantly, termination of transcription by RNA polymerase II on ins 5 DNA was also increased compared with wild-type virus; nearly 100% of the polymerases terminated per traverse of the ins 5 genome. These ***findings*** demonstrate that the rabbit .beta.-globin insert, which contains a strong ***polyadenylation*** ***signal*** , also contains at least part of a signal for termination of transcription by RNA polymerase II. The multiple, spliced leaders on polyomavirus L-strand mRNAs, which arise as a result of inefficient termination and polyadenylation, are not necessary for efficient virus replication.

L5 ANSWER 131 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1988:505719 CAPLUS
DN 109:105719
TI Complete cDNA sequence coding for the human T cell receptor .alpha. chain of HPB-ALL
AU Berkhout, Ben; Hall, Craig; Terhorst, Cox
CS Lab. Mol. Immunol., Dana-Farber Cancer Inst., Boston, MA, 02115, USA
SO Nucleic Acids Research (1988), 16(11), 5209 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB A .lambda.gt10 cDNA library was constructed using poly(A) RNA isolated from the human acute lymphocytic leukemia T cell line HPB-ALL. Four phages hybridizing to a T cell receptor (TCR) .alpha.-chain-specific probe were purified. The complete nucleotide sequence of the longest EcoRI insert was detd. It was found that the protein encoding sequences, including the variable region of the .alpha.-chain, were identical to the previously reported sequence of the TCR-.alpha. chain of the HPB-MLT cell line. Since the TCR-.beta. chains of both cell lines were also found to be identical, this ***finding*** supports the suggestion that the ALL and MLT cell lines are actually the same and may once have been confused during in vitro culturing. The 5' untranslated and translation initiation regions of the TCR-.alpha. mRNA are presented because these sequences were absent from the published MLT-.alpha. cDNA (Sim, G. K., et al., 1984). An mRNA leader of 99 nucleotides preceded two potential start codons, both of which only partially resembled the consensus site for translation initiation. Usage of the first ATG triplet will give a hydrophobic leader peptide of 23 amino acids. The 553-nucleotide-long 3'- untranslated sequences are similar to the genomic data and the cDNA ends 13 nucleotides following an ATTAAA ***polyadenylation*** ***signal*** .

L5 ANSWER 132 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1988:432969 CAPLUS
DN 109:32969
TI Complete sequence of cytochrome P450 3c cDNA and presence of two mRNA species with 3' untranslated regions of different lengths
AU Dalet, Christian; Clair, Philippe; Daujat, Martine; Fort, Philippe; Blanchard, Jean Marie; Maurel, Patrick
CS CNRS, Montpellier, 34033, Fr.
SO DNA (1988), 7(1), 39-46 CODEN: DNAADR; ISSN: 0198-0238
DT Journal
LA English
AB Two cDNAs (pLM3c 4.1 and pLM3c 6.1) coding for rabbit cytochrome P 450 3c were sequenced. The cDNA 4.1 (1768 bp) exhibits an open reading frame from nucleotides 74 to 1576 encoding the 501 amino acid residues of the entire protein. The cDNA 6.1 (189 bp) appears to encode the last 24 amino acids. Comparative amino acid sequence anal. indicated that P 450 PCN1, PCN2, and HLp from rat and man, were 70, 67, and 73% homologous, resp., to P 450 3c. According to the cytochrome P 450 nomenclature, the P 450 3c gene is termed P450IIIA4. Comparison of the nucleotide sequences indicated that cDNA 6.1 was 100% homologous to cDNA 4.1. However, whereas a poly(A) tract started 23 nucleotides after the AATAAA consensus sequence in cDNA 6.1, cDNA 4.1 had a 3' untranslated region extending 101 bp beyond the ***polyadenylation*** ***signal*** , which lacked poly(A). This observation is consistent with the previous ***finding*** that both cDNA 4.1 and 6.1 hybridized with two distinct species of poly(A)RNA (1700 and 1850 bases) from rabbit liver. The extreme 3'-end 79-bp fragment of cDNA 4.1 therefore was isolated by subcloning in pUC12 (clone p18-Rsa I) and used to probe Northern blots of poly(A)RNA from control and rifampicin-treated rabbit liver. In contrast to cDNA 4.1 and 6.1, p18-Rsa I cDNA hybridized only with the largest (1850 bases) mRNA species. Thus, rabbit liver contains two P 450 3c mRNA species differing in the length of their 3' untranslated region.

L5 ANSWER 133 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1988:50537 CAPLUS
DN 108:50537
TI Putative ***polyadenylation*** ***signals*** in nuclear genes of higher plants: a compilation and analysis
AU Joshi, C. P.
CS Div. Biochem. Sci., Natl. Chem. Lab., Pune, 411 008, India
SO Nucleic Acids Research (1987), 15(23), 9627-40 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB In animal and viral pre-mRNAs, the process of polyadenylation is mediated through several cis-acting poly(A) signals present upstream and downstream from poly(A) sites. The situation regarding polyadenylation of higher plant pre-mRNAs, however, has remained obscure so far. A ***search*** for putative poly(A) signals was made by examg. the published data from 46 plant genomic DNA sequences. Certain domains in the 3' untranslated regions from nuclear genes of higher plants were compiled and the occurrence of sequence motifs such as AATAAA, CAYTG, YGTGTTYY, and YAYTG was scored in relation to poly(A) sites. Moreover, consensus sequences for important regions in the 3' untranslated sequences and poly(A) signals were also deduced from the data. It was inferred that sequence motifs similar to poly(A) signals exist around poly(A) sites, but some of them are in entirely different spatial relationship than obsd. in other eukaryotes. This indicates their probable non-involvement in the process of polyadenylation in higher plants, necessitating a functional anal. approach to define the plant specific poly(A) signals.

L5 ANSWER 134 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN

AN 1988:17121 CAPLUS
DN 108:17121
TI Analysis of cDNA clones that code for the transmembrane forms of the mouse neural cell adhesion molecule (NCAM) and are generated by alternative RNA splicing
AU Santoni, Marie Jose; Barthels, Dagmar; Barbas, Julio A.; Hirsch, Marie Rose; Steinmetz, Michael; Goridis, Christo; Wille, Wolfgang
CS Cent. Immunol., INSERM, Marseille, F-13288, Fr.
SO Nucleic Acids Research (1987), 15(21), 8621-41 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB The neural cell adhesion mol. (NCAM) exists in at least three different isoforms. In the mouse, NCAM proteins with apparent Mr's of 180,000; 140,000; and 120,000 have been distinguished. These are encoded by 4 to 5 different transcripts. The full amino acid sequence of an isoform which most likely represents NCAM-140 is reported. The N-terminal extracellular portion of the 829-residue polypeptide appears to be identical to all three NCAM proteins. The Mr of 91,276 is considerably smaller than the est. based on SDS-gel electrophoresis. The 147 C-terminal residues are distinct from NCAM-120 and contain the putative transmembrane and cytoplasmic domains. The transcript encoding NCAM-140 contains an almost 3.2 kb non-coding sequence with a canonical ***polyadenylation*** ***signal*** . While the 5' sequences of NCAM-140 hybridize with all NCAM mRNAs, the 3' probes recognize only the two larger transcripts of 7.4 and 6.7 kb. From S1 nuclease protection analyses and hybridization studies of several NCAM cDNA clones with genomic NCAM sequences, one can conclude that the different NCAM transcripts are generated by alternative splicing. In addn. to the two alternative splice sites in the sequence encoding the extracellular domains, a third one can be predicted approx. 320 nt downstream of the start of the NCAM-140-specific sequence portion. This ***finding*** is in agreement with the existence of an extra exon in the chicken NCAM-180. Comparison between mouse and chicken NCAM amino acid sequences revealed the highest homol. in the second and fifth Ig-like domains and in the cytoplasmic parts, suggesting that these regions serve highly conserved functions.

L5 ANSWER 135 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1987:630359 CAPLUS
DN 107:230359
TI Structure of yeast regulatory gene LEU3 and evidence that LEU3 itself is under general amino acid control
AU Zhou, Kemin; Brisco, Paula R. G.; Hinkkanen, Ari E.; Kohlhaw, Gunter B.
CS Dep. Biochem., Purdue Univ., West Lafayette, IN, 47907, USA
SO Nucleic Acids Research (1987), 15(13), 5261-73 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB Detn. of the nucleotide sequence of a DNA region from Saccharomyces cerevisiae previously shown to contain the LEU3 gene revealed one long open reading frame (ORF) whose 887 codons predict the existence of a protein with a mol. mass of 100,162 daltons. The codon bias index of 0.02 suggests that LEU3 encodes a low-abundance protein. The predicted amino acid sequence contains a stretch of 31 residues near the N-terminus that is rich is cysteines and basic amino acids and shows strong homol. to similar regions in five other regulatory proteins of lower eukaryotes. Addnl. regions with a predominance of basic amino acids are present adjacent to the cysteine-rich region. A stretch of 20 residues, 19 of which are glu or asp, is found in the carboxy terminal quarter of the protein. The 5' flanking region of LEU3 contains a TATA box 111 bp upstream from the beginning of the long ORF and two transcription initiation elements (5'TCAA3') 58 and 48 bp upstream from the ORF. The 3' flanking region shows a tripartite potential termination- ***polyadenylation*** ***signal*** . The predicted 5' and 3' ends of the transcript are in very good agreement with the previously detd. size of the LEU3 message. Anal. of a LEU3'-'lacZ translational fusion suggests that the LEU3 gene, whose product is involved in the specific regulation of the leucine and possibly the isoleucine-valine pathways, is itself under general amino acid control. Consistent with this observation is the ***finding*** that the 5' flanking region of LEU3 contains two perfect copies of the general control target sequence 5'TGACTC3'.

L5 ANSWER 136 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1987:528206 CAPLUS
DN 107:128206
TI Primary structure of human nuclear ribonucleoprotein particle C proteins: conservation of sequence and domain structures in heterogeneous nuclear RNA, mRNA, and pre-rRNA-binding proteins
AU Swanson, Maurice S.; Nakagawa, Terry Y.; LeVan, Kay; Dreyfuss, Gideon
CS Dep. Biochem., Mol. Biol. Cell Biol., Northwestern Univ., Evanston, IL, 60201, USA
SO Molecular and Cellular Biology (1987), 7(5), 1731-9 CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB In the eukaryotic nucleus, heterogeneous nuclear RNAs exist in a complex with a specific set of proteins to form heterogeneous nuclear ribonucleoprotein particles (hnRNPs). The C proteins, C1 and C2, are major constituents of hnRNPs and appear to play a role in RNA splicing, as suggested by antibody inhibition and immunodepletion expts. With the use of a partial cDNA clone as a hybridization probe, full-length cDNAs for the human C proteins were isolated. All of the cDNAs isolated hybridized to two poly(A)+ RNAs of 1.9 and 1.4 kilobases (kb). DNA sequencing of a cDNA clone for the 1.9-kb mRNA (pHC12) revealed a single open reading frame of 290 amino acids coding for a protein of 31,931 daltons and two ***polyadenylation*** ***signals*** , AAUAAA, .apprx.400 base pairs apart in the 3' untranslated region of the mRNA. DNA sequencing of a clone corresponding to the 1.4-kb mRNA (pHC5) indicated that the sequence of this mRNA is identical to that of the 1.9-kb mRNA up to the first ***polyadenylation*** ***signal*** which it uses. Both mRNAs, therefore, have the same coding capacity and are probably transcribed from a single gene. Translation in vitro of the 1.9-kb mRNA selected by hybridization with a 3'-end subfragment of pHC12 demonstrated that it by itself can direct the synthesis of both C1 and C2. The difference between the C1 and C2 proteins which results in their electrophoretic sepn. is not known, but most likely one of them is generated from the other posttranslationally. Since several hnRNP proteins appeared by SDS-polyacrylamide gel electrophoresis to be multiple antigenically related polypeptides, this raises the possibility that some of these other groups of hnRNP proteins are also each produced from a single mRNA. The predicted amino acid sequence of the protein indicates that it is composed of 2 distinct domains: an amino terminus that contains an RNP consensus sequence, which is the putative RNA-binding site, and a carboxy terminus that is very neg. charged, contains no arom. amino acids or prolines, and contains a putative nucleoside triphosphate-binding fold, as well as a phosphorylation site for casein kinase type II. The RNP consensus sequence was also found in the yeast poly(A)-binding protein (PABP), the

heterogeneous nuclear RNA-binding proteins A1 and A2, and the pre-rRNA binding protein C23. All of these proteins are also composed of at least 2 distinct domains: an amino terminus, which possesses one or more RNP consensus sequences, and a carboxy terminus, which is unique to each protein, being very acidic in the C proteins and rich in glycine in A1, A2, and C23 and rich in proline in the poly(A)-binding protein. These ***findings*** suggest that the amino terminus of these proteins possesses a highly conserved RNA-binding domain, whereas the carboxy terminus contains a region essential to the unique function and interactions of each of the RNA-binding proteins.

L5 ANSWER 137 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1986:584957 CAPLUS
DN 105:184957
TI Nucleotide sequence analysis of the long terminal repeat of integrated caprine arthritis encephalitis virus
AU Sherman, Levana; Gazit, Arnona; Yaniv, Abraham; Dahlberg, John E.; Tronick, Steven R.
CS Sackler Sch. Med., Tel Aviv Univ., Tel-Aviv, 69978, Israel
SO Virus Research (1986), 5(2-3), 145-55 CODEN: VIREDF; ISSN: 0168-1702
DT Journal
LA English
AB The nucleotide of the long terminal repeat (LTR) of caprine arthritis encephalitis virus (CAEV), a prototype lentivirus, was detd. Six-base-pair (bp) directly repeated host cell sequences flank the 376-bp proviral LTRs. By comparison with other retroviral sequences, the CAEV LTR likely contains U3, R, and U5 regions 207, 86, and 83 bp in length, resp. Sequences conforming to consensus transcriptional promoter sites were identified in the U3 region upstream of a potential transcription initiation site. A consensus ***polyadenylation*** ***signal*** is present 20 bp upstream of the putative R-U5 border and a potential poly(A)-addn. site. Sequence comparisons of the CAEV LTR with those of other retroviruses uncovered significant similarities with that of visna virus. No other global homologies with other retrovirus LTRs could be detected. CAEV utilizes a primer binding site complementary to lysine tRNA as does visna, AIDS-assocd. retroviruses, and mouse mammary tumor virus. The putative primer for pos.-strand DNA synthesis identified in the CAEV sequence is identical to that of visna virus and very similar to those of AIDS retroviruses and MMTV. In addn., a stretch that includes that TATA box of the CAEV LTR resembles closely the corresponding region in the AIDS retrovirus. These and other ***findings*** further strengthen the classification of AIDS retrovirus as a lentivirus.

L5 ANSWER 138 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1986:492393 CAPLUS
DN 105:92393
TI Characteristic sequences in the 3' flanking region of wheat histone genes
AU Tabata, Tetsuya; Iwabuchi, Masaki
CS Fac. Sci., Hokkaido Univ., Hokkaido, 060, Japan
SO Plant and Cell Physiology (1986), 27(5), 929-33 CODEN: PCPHA5; ISSN: 0032-0781
DT Journal
LA English
AB The 3' flanking sequences of the coding regions of 3 wheat histone genes (1 H3 and 2 H4 genes) were examd. in an attempt to ***find*** signal sequences involved in regulating the transcription of the histone genes. A characteristic sequence, 5'(T)n(G)m--TG--AT3', was found in the vicinity of the region at which the 3' end of the wheat histone mRNA was mapped. This sequence was different from the ***polyadenylation*** ***signal*** or dyad symmetry structure that is common to animal histone genes.

L5 ANSWER 139 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1985:417708 CAPLUS
DN 103:17708
TI Thalassemia due to a mutation in the cleavage-***polyadenylation*** ***signal*** of the human .beta.-globin gene
AU Orkin, Stuart H.; Cheng, Tu Chen; Antonarakis, Stylianos E.; Kazazian, Haig H., Jr.
CS Div. Hematol.-Oncol., Childrens Hosp., Boston, MA, 02115, USA
SO EMBO Journal (1985), 4(2), 453-6 CODEN: EMJODG; ISSN: 0261-4189
DT Journal
LA English
AB A .beta.-globin gene cloned from a person with .beta.-thalassemia contained a T .fwdarw. C substitution within the conserved sequence AATAAA that forms a portion of the recognition signal for endonucleolytic cleavage and polyadenylation of primary mRNA transcripts. By Northern blot anal., a novel .beta.-globin RNA species, 1500 nucleotides in length, was detected in erythroid RNA. Nuclease protection studies of erythroid RNA, as well as RNA generated upon transient expression of the cloned mutant gene in HeLa cells, located the 3' terminus of this novel, polyadenylated RNA 900 nucleotides downstream of the normal poly(A)-addn. site, within 15 nucleotides of the 1st AATAAA in the 3'-flanking region of the .beta.-globin gene. These ***findings*** define the in vivo terminus of an elongated RNA and establish that human .beta.-globin transcription may extend .gtoreq.900 nucleotides 3' of the normal polyadenylation site.

L5 ANSWER 140 OF 140 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1985:161441 CAPLUS
DN 102:161441
TI Molecular genetics of a transposon-induced dominant mutation in the Drosophila locus Glued
AU Swaroop, Anand; Paco-Larson, M. Luisa; Garen, Alan
CS Dep. Mol. Biophys. Biochem., Yale Univ., New Haven, CT, 06511, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1985), 82(6), 1751-5 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The organization of the Drosophila locus Glued contg. the dominant allele Gl differed from that of the normal locus by an insertion of a 9-klobase-pair DNA segment near the 3' end of a transcribed region. The insertion causes the formation of a truncated polyadenylated transcript of 5.1 kilobases instead of the normal 6.0 kilobases. The inserted DNA segment has the properties of a transposon and was identified by its corresponding restriction map as B104, which is a retrovirus-like transposon with direct terminal repeats. B104 Appears to be oriented in Gl with the same polarity of transcription as Gl. The truncated Gl transcript terminates prematurely inside the 5'-terminal repeat of B104, in the region of a putative ***polyadenylation*** ***signal*** . The general implications of this ***finding*** are discussed for transposon- and retrovirus-induced mutagenesis and for the origin of dominant mutations.

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